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(54) Title: NUCLEIC ACID ENCODING NEUROPEPTIDE Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF (57) Abstract <p>This invention provides isolated nucleic acid molecules encoding Y2 receptors, an isolated, purified Y2 receptor protein, vectors comprising isolated nucleic acid molecules encoding Y2 receptors, mammalian, insect, bacterial and yeast cells comprising such vectors, antibodies directed to the Y2 receptors, nucleic acid probes useful for detecting nucleic acid encoding Y2 receptors, antisense oligonucleotides complementary to unique sequences of a nucleic acid molecule which encodes a Y2 receptor, pharmaceutical compounds related to the Y2 receptors, and nonhuman transgenic animals which express nucleic acid encoding a normal or mutant Y2 receptor. This invention further provides methods for determining ligand binding, detecting expression, drug screening, and methods of treatment involving Y2 receptors.</p>		

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**NUCLEIC ACID ENCODING NEUROPEPTIDE Y/PEPTIDE YY (Y2)
RECEPTORS AND USES THEREOF**

Background of the Invention

- 5 This application is a continuation-in-part of U.S. Serial No. 08/192,288, filed February 3, 1994, the contents of which are hereby incorporated by reference into the subject application.
- 10 Throughout this application, various publications are referenced in parenthesis by number. Full citations for these references may be found at the end of the specification immediately preceding the claims. The disclosure of these publications is hereby incorporated
- 15 by reference into this application to describe more fully the art to which this invention pertains.

Neuropeptides are small peptides originating from large precursor proteins synthesized by peptidergic neurons and

20 endocrine/paracrine cells. They hold promise for treatment of neurological, psychiatric, and endocrine disorders (46). Often the precursors contain multiple biologically active peptides. There is great diversity of neuropeptides in the brain caused by alternative

25 splicing of primary gene transcripts and differential precursor processing. The neuropeptide receptors serve to discriminate between ligands and to activate the appropriate signals.

- 30 Neuropeptide Y (NPY), a 36-amino acid peptide, is the most abundant neuropeptide to be identified in mammalian brain. NPY is an important regulator in both the central and peripheral nervous systems (47) and influences a diverse range of physiological parameters, including
- 35 effects on psychomotor activity, food intake, central endocrine secretion, and vasoactivity in the

cardiovascular system. High concentrations of NPY are found in the sympathetic nerves supplying the coronary, cerebral, and renal vasculature and have contributed to vasoconstriction. NPY binding sites have been identified
5 in a variety of tissues, including spleen (48), intestinal membranes, brain (49), aortic smooth muscle (50), kidney, testis, and placenta (2). In addition, binding sites have been reported in a number of rat and human cell lines (e.g. Y1 in SK-N-MC, MC-IXC, CHP-212,
10 and PC12 cells; Y2 in SK-N-Be(2), CHP-234, and SMS-MSN) (51,5).

Neuropeptide Y (NPY) receptor pharmacology is currently defined by structure activity relationships within the
15 pancreatic polypeptide family (1, 2). This family includes NPY, which is synthesized primarily in neurons; peptide YY (PYY), which is synthesized primarily by endocrine cells in the gut; and pancreatic polypeptide (PP), which is synthesized primarily by endocrine cells
20 in the pancreas. These 36 amino acid peptides have a compact helical structure involving a "PP-fold" in the middle of the peptide. Specific features include a polyproline helix in residues 1 through 8, a β -turn in residues 9 through 14, an α -helix in residues 15 through
25 30, an outward-projecting C-terminus in residues 30 through 36, and a carboxyl terminal amide which appears to be critical for biological activity (3). The peptides have been used to define at least four receptor subtypes known as Y1, Y2, Y3, and PP. Y1 receptor recognition by
30 NPY involves both N- and C-terminal regions of the peptide; exchange of Gln³⁴ with Pro³⁶ is fairly well tolerated (3, 4, 5). Y2 receptor recognition by NPY depends primarily upon the four C-terminal residues of the peptide (Arg³³-Gln³⁴-Arg³⁵-Tyr³⁶-NH₂) preceded by an
35 amphipathic α -helix (3, 6, 7); exchange of Gln³⁴ with Pro³⁶ is not well tolerated (4, 5). Y3 receptor recognition is characterized by a strong preference for NPY over PYY

(8). Exchange of Gln³⁴ in NPY with Pro³⁴ is reasonably well tolerated by the Y3 receptor but PP, which also contains Pro³⁴, does not bind well (8). The PP receptor is reported to bind tightly to PP, less so to [Leu³¹,Pro³⁴]NPY, and even less so to NPY (3, 9). The only NPY receptor which has been cloned to date is the Y1 receptor gene, from mouse (12), rat (52), and human (10). One of the key pharmacological features which distinguish Y1 and Y2 is the fact that the Y1 receptor (and not the Y2 receptor) responds to an analog of NPY modified at residues 31 and 34 ([Leu³¹,Pro³⁴]NPY), whereas the Y2 receptor (and not the Y1 receptor) has high affinity for the NPY peptide carboxyl-terminal fragment NPY-(13-36) (53,4).

Receptor genes for the other two structurally related peptides, peptide YY (PYY) and pancreatic polypeptide (PP), also have not been cloned. Peptide YY occurs mainly in endocrine cells in the lower gastrointestinal tract (54). Receptors for PYY were first described in the rat small intestine (55). This receptor has been defined as PYY-preferring because it displays a 5-10 fold higher affinity for PYY than for NPY (55,56). Recently, a cell line, PKSV-PCT, derived from the proximal tubules of kidneys, has been described to express receptors for PYY (57).

In the last few years only the rat and human Y1 cDNAs have been cloned (10, 11). This success was based on identifying the randomly cloned FC5 "orphan receptor" (12). We now report the isolation by expression cloning of a human hippocampal Y2 cDNA clone and two rat Y2 clones and their pharmacological characterization.

Summary of the Invention

This invention provides an isolated nucleic acid molecule encoding a Y2 receptor.

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This invention also provides an isolated protein which is a Y2 receptor.

This invention provides a vector comprising nucleic acid encoding a Y2 receptor.

10

This invention also provides vectors such as plasmids comprising nucleic acid encoding a Y2 receptor, adapted for expression in a bacterial cell, a yeast cell, an insect cell or a mammalian cell which additionally comprise the regulatory elements necessary for expression of the nucleic acid in the bacterial, yeast, insect or mammalian cells operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.

15
20

This invention provides a cell transfected with and expressing nucleic acid encoding a Y2 receptor.

This invention provides a nucleic acid probe comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a unique sequence included within the sequence of a nucleic acid molecule encoding a Y2 receptor.

25

This invention provides an antisense oligonucleotide having a sequence capable of specifically hybridizing with any sequences of an mRNA molecule which encodes a Y2 receptor so as to prevent translation of the mRNA molecule.

30
35

This invention provides an antibody directed to a Y2 receptor.

This invention provides a transgenic nonhuman mammal expressing nucleic acid encoding a Y2 receptor. This invention further provides a transgenic nonhuman mammal whose genome comprises antisense DNA complementary to DNA
5 encoding a Y2 receptor so placed as to be transcribed into antisense mRNA which is complementary to mRNA encoding a Y2 receptor and which hybridizes to mRNA encoding a Y2 receptor thereby reducing its translation.

10 This invention further provides a transgenic nonhuman mammal comprising a homologous recombination knockout of the native Y2 receptor.

This invention provides a method for determining whether
15 a ligand can bind specifically to a Y2 receptor which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting binding of ligands to such receptor, and detecting the presence of any such
20 ligand bound to the Y2 receptor, thereby determining whether the ligand binds specifically to a Y2 receptor.

This invention also provides a method for determining whether a ligand is a Y2 receptor agonist which comprises
25 contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting the activation of a functional Y2 receptor response from the cell, and detecting, by means of a bioassay, such as a second messenger assay, an
30 increase in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor agonist.

This invention further provides a method for determining whether a ligand is a Y2 receptor antagonist which
35 comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand in the presence of a known Y2 receptor agonist,

such as NPY, under conditions permitting the activation of a functional Y2 receptor response, and detecting, by means of a bioassay, such as a second messenger assay, a decrease in Y2 receptor activity, thereby determining
5 whether the ligand is a Y2 receptor antagonist.

This invention further provides a method of screening drugs to identify drugs which specifically bind to a Y2 receptor on the surface of a cell which comprises
10 contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs under conditions permitting binding of drugs to the Y2 receptor, and determining those drugs which bind to the Y2 receptor, thereby identifying drugs which specifically
15 bind to a Y2 receptor.

This invention also provides a method of screening drugs to identify drugs which act as agonists of a Y2 receptor on the surface of a cell which comprises contacting a
20 cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which activate the Y2 receptor, using a bioassay, such as a
25 second messenger assay, thereby identifying drugs which act as Y2 receptor agonists.

This invention also provides a method of screening drugs to identify drugs which act as antagonists of a Y2
30 receptor on the surface of a cell which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs in the presence of a known Y2 receptor agonist, such as NPY, under conditions permitting the activation of a
35 functional Y2 receptor response, and determining those drugs which inhibit the activation of the Y2 receptor, using a bioassay, such as a second messenger assay,

thereby identifying drugs which act as Y2 receptor antagonists.

This invention also provides a method of detecting expression of a Y2 receptor by a cell by detecting the presence of mRNA coding for the Y2 receptor which comprises obtaining total mRNA from the cell and contacting the mRNA so obtained with a nucleic acid probe comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a unique sequence included within the sequence of a nucleic acid molecule encoding the Y2 receptor under hybridizing conditions, and detecting the presence of mRNA hybridized to the probe, thereby detecting the expression of a Y2 receptor by the cell.

This invention provides a method of determining the physiological effects of expressing varying levels of Y2 receptors which comprises producing a transgenic nonhuman mammal expressing nucleic acid encoding a Y2 receptor whose levels of Y2 receptor expression are varied by use of an inducible promoter which regulates Y2 receptor expression.

This invention also provides a method of determining the physiological effects of expressing varying levels of Y2 receptors which comprises producing a panel of transgenic nonhuman animals each expressing nucleic acid encoding a Y2 receptor expressing nucleic acid and expressing a different amount of Y2 receptor.

This invention provides a method for diagnosing a predisposition to a disorder associated with the activity of a specific Y2 receptor allele which comprises: a. obtaining nucleic acid of subjects suffering from the disorder; b. performing a restriction digest of the nucleic acid with a panel of restriction enzymes; c.

electrophoretically separating the resulting nucleic acid fragments on a sizing gel; d. contacting the resulting gel with a nucleic acid probe capable of specifically hybridizing to nucleic acid encoding a Y2 receptor and
5 labeled with a detectable marker; e. detecting labeled bands which have hybridized to the nucleic acid encoding a Y2 receptor labelled with a detectable marker to create a unique band pattern specific to the nucleic acid of subjects suffering from the disorder; f. preparing
10 nucleic acid obtained for diagnosis by steps a-e; and g. comparing the unique band pattern specific to the nucleic acid of subjects suffering from the disorder from step e and the nucleic acid obtained for diagnosis from step f to determine whether the patterns are the same or
15 different and to diagnose thereby predisposition to the disorder if the patterns are the same.

This invention provides a method of preparing an isolated, purified Y2 receptor which comprises
20 constructing a vector adapted for expression in a cell which comprises the regulatory elements necessary for the expression of nucleic acid in the cell operatively linked to the nucleic acid encoding a Y2 receptor as to permit expression thereof, wherein the cell is selected from the
25 group consisting of bacterial cells, yeast cells, insect cells and mammalian cells; inserting the vector of the previous step in a suitable host cell; incubating the cells under conditions allowing the expression of a Y2 receptor; recovering the receptor so produced and
30 purifying the receptor so recovered.

Brief Description of the Drawings

Figure 1

- 5 Nucleotide sequence of the human hippocampal Y2 cDNA clone (SEQ. I.D. No. 1). Initiation and stop codon are indicated in bold. Only partial 5' and 3' untranslated sequences are shown.

10 Figure 2

Deduced amino acid sequence of the human hippocampal Y2 cDNA clone encoded by the nucleotide sequence in Figure 1 (SEQ. I.D. No. 2).

15 Figure 3-1 through Figure 3-4

Comparison of coding nucleotide sequences between human hippocampal Y2 (top row) and Y1 human cDNA clones (bottom row) (48.5% nucleotide identity).

20 Figure 4-1 and Figure 4-2

Comparison of amino acid sequences between hippocampal Y2 (top row) and Y1 human cDNA clones (bottom row). (31% overall identity and 41% in the transmembrane domains).

25 Figure 5A

- Equilibrium binding of ^{125}I -PYV to membranes from COS-7 cells transiently expressing CG-13 (•) and human Y1 (○) receptors. Membranes were incubated with ^{125}I -PYV for the times indicated, in the presence or absence of 100 nM human NPY. Specific binding, B , was plotted against time, t , to obtain the maximum number of equilibrium binding sites, B_1 and B_2 , and observed association rates, $K_{\text{obs}1}$ and $K_{\text{obs}2}$, according to the equation, $B = B_1 * (1 - e^{-(k_{\text{obs}1} * t)}) + B_2 * (1 - e^{-(k_{\text{obs}2} * t)})$. Binding is shown as the
- 30 percentage of total equilibrium binding, $B_1 + B_2$, determined by nonlinear regression analysis. Data are representative of three independent experiments, with

each point measured in triplicate.

Figure 5B

Equilibrium binding of ^{125}I -PYV to membranes from COS-7
5 cells transiently expressing CG-13 (•) and human Y1 (○)
receptors using the same conditions as in Figure 5A
except for a prolonged time course of up to 180 minutes.

Figure 6

10 Saturable equilibrium binding of ^{125}I -PYV to membranes from
COS-7 cells transiently expressing CG-13 receptors.
Membranes were incubated with ^{125}I -PYV ranging in
concentration from 0.003 nM to 2 nM, in the presence or
absence of 100 nM human NPY. Specific binding, B, was
15 plotted against the free ^{125}I -PYV concentration, [L], to
obtain the maximum number of saturable binding sites, B_{max} ,
and the ^{125}I -PYV equilibrium dissociation constant, K_d ,
according to the binding isotherm, $B = B_{\text{max}}[L]/([L] + K_d)$.
Specific binding is shown. Data are representative of
20 three independent experiments, with each point measured
in triplicate.

Figure 7A

Competitive displacement of ^{125}I -PYV on membranes from COS-
25 7 cells transiently expressing Human Y1 receptors.
Membranes were incubated with ^{125}I -PYV and increasing
concentrations of peptide competitors. IC_{50} values
corresponding to 50% displacement were determined by
nonlinear regression analysis and converted to K_i values
30 according to the equation, $K_i = \text{IC}_{50}/(1 + [L]/K_d)$, where
[L] is the ^{125}I -PYV concentration and K_d is the equilibrium
dissociation constant of ^{125}I -PYV. Data are representative
of at least two independent experiments, with each point
measured once or in duplicate. Rank orders of affinity
35 for these and other compounds are listed separately in
Table 2.

Figure 7B

Competitive displacement of ^{125}I -PYV on membranes from COS-7 cells transiently expressing human Y2 receptors. Membranes were incubated with ^{125}I -PYV and increasing concentrations of peptide competitors. IC_{50} values corresponding to 50% displacement were determined by nonlinear regression analysis and converted to K_i values according to the equation, $K_i = \text{IC}_{50}/(1 + [\text{L}]/K_d)$, where $[\text{L}]$ is the ^{125}I -PYV concentration and K_d is the equilibrium dissociation constant of ^{125}I -PYV. Data are representative of at least two independent experiments, with each point measured once or in duplicate. Rank orders of affinity for these and other compounds are listed separately in Table 2.

15

Figure 8 Nucleotide sequence (SEQ. I.D. No. 3) and deduced amino acid sequence (SEQ. I.D. No. 4) of the rat Y2 receptor encoded by rs5a. Nucleotides are presented in the 5' to 3' orientation and the coding region is numbered starting from the putative initiating methionine and ending in the termination codon. Deduced amino acid sequence by translation of a long open reading frame is shown using one-letter symbols.

20

Figure 9 Nucleotide sequence (SEQ. I.D. No. 5) and deduced amino acid sequence (SEQ. I.D. No. 6) of the rat Y2 receptor encoded by rs26a. Nucleotides are presented in the 5' to 3' orientation and the coding region is numbered starting from the putative initiating methionine and ending in the termination codon. Deduced amino acid sequence by translation of a long open reading frame is shown using one-letter symbols.

30

Figure 10 Alignment of rat and human Y2 receptors: nucleotide sequences. Nucleotide sequences of the coding regions of the human Y2 receptor (HumY2) and the rat Y2 receptors encoded by rs5a (RatY2a) and rs26a (RatY2b) are

35

shown; the nucleotide sequence of rs26a (RatY2b) is identical to rs5a (RatY2a) except where shown. Rat and human Y2 nucleotide sequences exhibit ~86% identity in the coding region.

5

Figure 11 Alignment of rat and human Y2 receptors: amino acid sequences. Complete predicted amino acid sequences of the human Y2 receptor (Hum Y2) and the rat Y2 receptor encoded by rs5a (Rat Y2a) are shown; the amino acid sequence of RatY2b encoded by rs26a is identical to RatY2a except where shown. Rat and human Y2 amino acid sequences are ~94% identical overall and ~98% identical in the transmembrane domains (bracketed). Single letter abbreviations for amino acids are shown.

15

Figure 12 Localization of Rat Y2 mRNA in the rat central nervous system. Schematic diagrams of half-coronal sections through the rat brain showing the distribution of neuropeptide Y Y2 receptor mRNA obtained with radiolabelled oligonucleotide probes and in situ hybridization histochemistry. The stars show the location of labeled neuronal populations, and are not indicative of the number of cells observed in each area.

25

Figure 13 Effects of Gpp(NH)p on radio ligand binding to Y2 receptors. Binding data were generated from competitive displacement assays in the absence (•) or presence (○) of 100 μ M Gpp(NH)p. The maximum specific binding detected under control conditions (in the absence of Gpp(NH)p) was used to normalize the data. A) Human Y2 receptor transiently expressed in COS-7 cells. B) Rat Y2a receptor transiently expressed in COS-7 cells.

35

Figure 14 Inhibition of forskolin-stimulated cAMP accumulation in intact cells stably expressing the human Y2 receptor. Functional data were derived from

radioimmunoassay of cAMP in 293 cells stimulated with 10 μ M forskolin over a 5 min period. Human PYY was tested for agonist activity over the same period. Data were fit to a four parameter logistic equation by nonlinear regression. Data generated from stably transfected 293 cells (•) and from stably transfected NIH-3T3 cells (○). Data shown are representative of ten (•) and two (○) independent experiments.

10 Figure 15 Stimulation of intracellular free calcium concentration in intact 293 cells stably expressing the human Y2 receptor. A) Time course. Functional data were derived from Fura-2/AM fluorescence in 293 cells stimulated with 1 μ M human PYY at the time indicated by the arrow. B) Time course. Cells were stimulated with 1 μ M human PYY as in A except that 1 mM EGTA was included in the extracellular solution. C) Concentration/response curve for PYY-dependent mobilization of intracellular calcium in 293 cells stably transfected with the human Y2 receptor. Data were fit to a four parameter logistic equation by nonlinear regression. Data shown are representative of at least two independent experiments.

25 Figure 16. Northern analysis of various human brain areas. Hybridization was done under conditions of high stringency, as described in Experimental Details. The probe was a 32 P-labeled DNA fragment (specific activity 3×10^9 cpm/ μ g) corresponding to the entire coding region (as shown in Figure 10) of the human NPY Y2 receptor. The BRL RNA ladder was used as molecular weight markers.

35 Figure 17. Southern analysis of genomic DNA encoding the human NPY Y2 receptor subtype. Hybridization was done under conditions of high stringency, as described in Experimental Details. The probe was a 32 P-labeled DNA fragment (specific activity 2.5×10^9 cpm/ μ g)

corresponding to the TM1-TM5 region of the human NPY Y2 receptor (as shown in Figure 11). Hind III digested λ DNA was used as molecular weight markers.

- 5 Figure 18. Photomicrographs showing some of the controls
used for NPY Y2 oligonucleotide probe specificity (A, B),
and tissue distribution of the hybridization signal in
rat brain (C, D). A. Darkfield photomicrograph of the
hybridization signal obtained using the radiolabeled
10 antisense probe on COS-7 cells transfected with the rat
Y2 DNA. B. Hybridization signal obtained following
hybridization with the radiolabeled sense probe, also on
transfected COS-7 cells. Only the antisense probes
hybridize to the transfected cells. C. Brightfield
15 photomicrograph of the hybridization signal observed in
the CA3 region of the rat hippocampus. Silver grains are
found over neuronal cell bodies (arrows) in the pyramidal
cell layer (sp), but not over the stratum lucidum (slu)
or stratum radiatum (sr). D. Hybridization signal
20 observed over neurons (arrows) in the arcuate nucleus of
the hypothalamus. The darkly stained ependymal lining of
the third ventricle can be seen to the left of the
micrograph (asterisk).

Detailed Description of the Invention

Throughout this application, the following standard abbreviations are used to indicate specific nucleotide
5 bases:

C = cytosine	A = adenine
T = thymine	G = guanine

This invention provides isolated nucleic acid molecules
10 which encode Y2 receptors. In one embodiment, the Y2 receptor encoded is a human Y2 receptor. In another embodiment, the Y2 receptor encoded is a rat Y2 receptor. As used herein, the term Y2 receptor encompasses any amino acid sequence, polypeptide or protein having
15 substantially the same pharmacology provided for the subject human Y2 receptor as shown in Tables 2-4 and Figures 5A-7B. As described herein our cloned receptor has a Y2 pharmacological profile that differs from the NPY receptor subtypes Y1 and Y3, PYY receptor, and PP
20 receptor, and is therefore designated as the Y2 receptor.

The only NPY receptor which has been cloned to date is the Y1 receptor gene, from mouse (Eva et al., 1992), rat (Eva et al., 1990), and human (Larhammar et al., 1992).
25 The human Y2 receptor's greatest homology with any known receptor disclosed in the Genbank/EMBL databases is a 42% overall amino acid identity with the human Y1 receptor.

This invention provides isolated nucleic acid molecules
30 encoding Y2 receptors. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. As used herein, the term "isolated nucleic acid molecule" means a nucleic acid molecule that is a molecule in a form which does not
35 occur in nature. Examples of such an isolated nucleic acid molecule are an RNA, cDNA, or isolated genomic DNA molecule encoding a Y2 receptor. The human Y2 receptor

has an amino acid sequence substantially the same as the deduced amino acid sequence shown in Figure 2 and any human receptor having substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 is by definition a human Y2 receptor. The rat Y2 receptor has an amino acid sequence substantially the same as the deduced amino acid sequences shown in Figure 8 or Figure 9. One means of isolating another Y2 receptor is to probe a genomic library with a natural or artificially designed DNA probe, using methods well known in the art. DNA probes derived from the human and the rat receptor Y2 gene are particularly useful probes for this purpose. DNA and cDNA molecules which encode Y2 receptors may be used to obtain genomic DNA, cDNA or RNA from human, mammalian or other animal sources, or to isolate related cDNA or genomic clones by the screening of cDNA or genomic libraries by methods described in more detail below. Transcriptional regulatory elements from the 5' untranslated region of the isolated clones, and other stability, processing, transcription, translation, and tissue specificity-determining regions from the 3' and 5' untranslated regions of the isolated genes are thereby obtained. Examples of a nucleic acid molecule are an RNA, cDNA, or isolated genomic DNA molecule encoding a Y2 receptor. Such molecules may have coding sequences substantially the same as the coding sequences shown in Figures 1, 8 and 9. The DNA molecule of Figure 1 encodes the sequence of the human Y2 receptor gene. The DNA molecules of Figures 8 and 9 encode the sequence of two rat Y2 receptor genes.

This invention further provides DNA molecules encoding Y2 receptors having coding sequences substantially the same as the coding sequences shown in Figures 1, 8 and 9. These molecules are obtained by the means described above.

This invention also provides an isolated nucleic acid molecule encoding a Y2 receptor wherein the nucleic acid molecule encodes a receptor being characterized by an amino acid sequence in the transmembrane region, which amino acid sequence has 60% homology or higher to the amino acid sequence in the transmembrane region of the human Y2 receptor as shown in Figure 11.

This invention also provides purified isolated proteins which are Y2 receptors. In one embodiment, the Y2 receptor protein is a human Y2 receptor protein. In another embodiment, the Y2 receptor protein is a rat Y2 receptor protein. As used herein, the term "isolated protein" means a protein molecule free of other cellular components. Examples of such proteins are isolated proteins having substantially the same amino acid sequence as the amino acid sequences shown in Figures 2, 8, and 9, which are a human Y2 receptor and two rat Y2 receptors, respectively. One means for obtaining an isolated Y2 receptor is to express DNA encoding the receptor in a suitable host, such as a bacterial, yeast, insect or mammalian cell, using methods well known in the art, and recovering the receptor protein after it has been expressed in such a host, again using methods well known in the art. The receptor may also be isolated from cells which express it, in particular from cells which have been transfected with the expression vectors described below in more detail.

This invention provides vectors comprising nucleic acid molecules such as DNA, RNA, or cDNA encoding Y2 receptors. In one embodiment, the nucleic acid encodes a human Y2 receptor. In another embodiment, the nucleic acid encodes a rat Y2 receptor. Examples of vectors are viruses such as bacteriophages (such as phage lambda), animal viruses (such as Herpes virus, Murine Leukemia virus, and Baculovirus), cosmids, plasmids (such as

pUC18, available from Pharmacia, Piscataway, NJ), and other recombination vectors. Nucleic acid molecules are inserted into vector genomes by methods well known in the art. For example, insert and vector DNA can both be
5 exposed to a restriction enzyme to create complementary ends on both molecules which base pair with each other and are then ligated together with a ligase. Alternatively, linkers can be ligated to the insert DNA which correspond to a restriction site in the vector DNA,
10 which is then digested with the restriction enzyme which cuts at that site. Other means are also available. Specific examples of such plasmids are: a plasmid comprising cDNA having a coding sequence substantially the same as the coding sequence shown in Figure 1 and
15 designated clone CG-13 (Seq. I.D. No. 1); or a plasmid comprising genomic DNA having a coding sequence substantially the same as the coding sequence shown in Figure 8 and designated clone rS5a (Seq. I.D. No. 3), or the coding sequence shown in Figure 9 and designated
20 clone rS26a (Seq. I.D. No. 5).

This invention also provides vectors comprising nucleic acid molecules encoding Y2 receptors, adapted for expression in a bacterial cell, a yeast cell, an insect
25 cell or a mammalian cell which additionally comprise the regulatory elements necessary for expression of the nucleic acid in the bacterial, yeast, insect or mammalian cells operatively linked to the nucleic acid encoding a Y2 receptor as to permit expression thereof. Nucleic acid
30 having coding sequences substantially the same as the coding sequence shown in Figure 1 may be usefully inserted into the vectors to express human Y2 receptors. Nucleic acid having coding sequences substantially the same as the coding sequences shown in Figures 8 and 9 may
35 be usefully inserted into vectors to express rat Y2 receptors. Regulatory elements required for expression include promoter sequences to bind RNA polymerase and

transcription initiation sequences for ribosome binding. For example, a bacterial expression vector includes a promoter such as the lac promoter and for transcription initiation the Shine-Dalgarno sequence and the start
5 codon AUG (Maniatis, et al., Molecular Cloning, Cold Spring Harbor Laboratory, 1982). Similarly, a eukaryotic expression vector includes a heterologous or homologous promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a
10 termination codon for detachment of the ribosome. Furthermore, an insect expression vector, such as recombinant baculovirus, uses the polyhedron gene expression signals for expression of the inserted gene in insect cells. Such vectors may be obtained commercially
15 or assembled from the sequences described by methods well known in the art, for example the methods described above for constructing vectors in general. Expression vectors are useful to produce cells that express the receptor. Certain uses for such cells are described in more detail
20 below.

This invention further provides a plasmid adapted for expression in a bacterial cell, a yeast cell, an insect cell, or, in particular, a mammalian cell which comprises
25 a nucleic acid molecule encoding a Y2 receptor and the regulatory elements necessary for expression of the nucleic acid in the bacterial, yeast, insect, or mammalian cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
30 In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. Some plasmids adapted for expression in a mammalian cell are pSVL (available from Pharmacia, Piscataway, NJ) and pcEXV-3 (73). One specific example
35 of such a plasmid is a plasmid adapted for expression in a mammalian cell comprising cDNA having a coding sequence substantially the same as the coding sequence shown in

Figure 1 and the regulatory elements necessary for expression of the DNA in the mammalian cell which is designated pcEXV-hY2, deposited on January 27, 1994 under ATCC Accession No. 75659. Other specific examples of such plasmids are plasmids adapted for expression in a mammalian cell comprising genomic DNA having coding sequences substantially the same as the coding sequences shown in Figures 8 and 9 and the regulatory elements necessary for expression of the DNA in the mammalian cell which are designated pcEXV-rY2a, deposited on January 25, 1995 under ATCC Accession No. 97035; and pcEXV-rY2b, deposited on January 25, 1995 under ATCC Accession No. 97036, respectively. Those skilled in the art will readily appreciate that numerous plasmids adapted for expression in a mammalian cell which comprise DNA encoding Y2 receptors and the regulatory elements necessary to express such DNA in the mammalian cell may be constructed utilizing existing plasmids and adapted as appropriate to contain the regulatory elements necessary to express the DNA in the mammalian cell. The plasmids may be constructed by the methods described above for expression vectors and vectors in general, and by other methods well known in the art.

The deposits discussed supra, and the other deposits discussed herein, were made pursuant to, and in satisfaction of, the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852.

This invention provides a cell transfected with and expressing nucleic acid encoding a Y2 receptor. In one embodiment the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. An example of such a cell is a mammalian cell transfected

with a plasmid adapted for expression in a mammalian cell, which comprises nucleic acid encoding a Y2 receptor, and the regulatory elements necessary for expression of the nucleic acid in the mammalian cell operatively linked
5 to the nucleic acid encoding a Y2 receptor as to permit expression thereof; the protein encoded thereby expressed on the cell surface. Numerous mammalian cells may be used as hosts, including, for example, the mouse fibroblast cell NIH-3T3, CHO cells, HeLa cells, LM(tk-)
10 cells, etc. Expression plasmids such as that described supra may be used to transfect cells by methods well known in the art such as calcium phosphate precipitation, or DNA encoding these Y2 receptors may be otherwise introduced into cells, e.g., by microinjection, to obtain
15 mammalian cells which comprise nucleic acid, e.g., cDNA or a plasmid, encoding a Y2 receptor. A specific example of such cells is a cell comprising the pcEXV-hY2 plasmid adapted for expression in a mammalian cell comprising cDNA encoding the Y2 receptor and the
20 regulatory elements necessary for expression of the DNA in the mammalian cell, which is designated 293-hY2-10 and deposited on January 27, 1994 under ATCC Accession No. 11837. Another specific example of such cells is a cell comprising the pcEXV-hY2 plasmid adapted for expression
25 in a mammalian cell comprising cDNA encoding the Y2 receptor and the regulatory elements necessary for expression of the DNA in the mammalian cell, which is designated N-hY2-5 and deposited on January 25, 1995 under ATCC Accession No. CRL-11825.

30

This invention provides a method for determining whether a ligand can bind specifically to a Y2 receptor which comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor, the
35 protein encoded thereby is expressed on the cell surface, with the ligand under conditions permitting binding of ligands known to bind to the Y2 receptor, and detecting

the presence of any of the ligand bound to the Y2 receptor, thereby determining whether the ligand binds specifically to the Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another
5 embodiment, the Y2 receptor is a rat Y2 receptor.

This invention further provides a method for determining whether a ligand can bind specifically to a Y2 receptor, which comprises contacting a cell transfected with and
10 expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting binding of ligands to such receptor, and detecting the presence of any such ligand bound to the Y2 receptor, wherein the Y2 receptor is characterized by an amino acid sequence in the
15 transmembrane region, such amino acid sequence having 60% homology or higher to the amino acid sequence in the transmembrane region of the Y2 receptor shown in Figure 11. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a
20 rat Y2 receptor.

This invention provides a method for determining whether a ligand can bind specifically to a Y2 receptor which comprises preparing a cell extract from cells transfected
25 with and expressing nucleic acid encoding a Y2 receptor, isolating a membrane fraction from the cell extract, contacting the ligand with the membrane fraction from the cell extract under conditions permitting binding of ligands to such receptor, and detecting the presence of
30 any ligand bound to the Y2 receptor, thereby determining whether the compound is capable of binding specifically to a Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

35

This invention also provides a method for determining whether a ligand is a Y2 receptor agonist. As used

herein, the term "agonist" means any ligand capable of increasing Y2 receptor functional activity. This comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with the
5 ligand under conditions permitting the activation of a functional Y2 receptor response from the cell, and detecting, by means of a bioassay, such as a second messenger assay, an increase in Y2 receptor activity, thereby determining whether the ligand acts as a Y2
10 receptor agonist. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

This invention further provides a method for determining
15 whether a ligand is a Y2 receptor agonist which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding a Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction of the extract with the ligand under
20 conditions permitting the activation of a functional Y2 receptor response, and detecting, by means of a bioassay, such as a second messenger assay, an increase in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor agonist. In one embodiment, the Y2
25 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

This invention also provides a method for determining whether a ligand a Y2 receptor antagonist. As used
30 herein, the term "antagonist" means any ligand capable of decreasing Y2 receptor functional activity. This comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with the ligand in the presence of a known Y2 receptor agonist
35 such as NPY, under conditions permitting the activation of a functional Y2 receptor response, and detecting, by means of a bioassay, such as a second messenger assay, a

decrease in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor antagonist. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

5

This invention also provides a method for determining whether a ligand is a Y2 receptor antagonist which comprises preparing a cell extract from cells transfected
10 with and expressing nucleic acid encoding a Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction of the extract with the ligand in the presence of a known Y2 receptor agonist, such as NPY, under conditions permitting the activation
15 of a functional Y2 receptor response, and detecting, by means of a bioassay, such as a second messenger assay, a decrease in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor antagonist. In one embodiment, the Y2 receptor is a human Y2 receptor. In
20 another embodiment, the Y2 receptor is a rat Y2 receptor.

In one embodiment, the second messenger assays referred to comprise measurement of intracellular cAMP. In another embodiment, the second messenger assays comprise
25 measurement of intracellular calcium mobilization.

In one embodiment, the nucleic acid in the cells referred to above encodes a Y2 receptor having an amino acid sequence substantially the same as the amino acid
30 sequence shown in Figure 2. In another embodiment, the nucleic acid in the cells referred to above encodes a Y2 receptor having an amino acid sequence substantially the same as the amino acid sequences shown in Figure 8 or Figure 9. In one embodiment, the cell is a mammalian
35 cell. Preferably, the mammalian cell is non-neuronal in origin. An example of a nonneuronal mammalian cell is a COS-7 cell. Other examples of a non-neuronal mammalian

cells that can be used for functional assays with Y2 receptors are the 293 human embryonic kidney cells, mouse embryonic fibroblast NIH-3T3 cells, and LM(tk-) cells.

- 5 The preferred method for determining whether a ligand is capable of binding specifically to a Y2 receptor comprises contacting a transfected nonneuronal mammalian cell (i.e. a cell that does not naturally express any type of NPY, PP, or PYY receptor, and thus will only
- 10 express such a receptor if it is transfected into the cell) expressing a Y2 receptor on its surface, or contacting a membrane preparation derived from such a transfected cell, with the ligand under conditions which are known to prevail, and thus to be associated with, in
- 15 vivo binding of the ligand to and/or activation of a Y2 receptor, and detecting the presence of any of the ligand being tested bound to the Y2 receptor on the surface of the cell, or detecting activation of the Y2 receptor, thereby determining whether the ligand binds to,
- 20 activates or inhibits the activation of the Y2 receptor. Activation of a Y2 receptor may be detected by means of a second messenger assay. Such a response system is obtained by transfection of nucleic acid into a suitable host cell containing the desired second messenger system
- 25 such as phospholipase C, adenylate cyclase, guanylate cyclase or ion channels. A suitable host cell can be isolated from pre-existing cell lines, or can be generated by inserting appropriate components of second messenger systems into existing cell lines. Such a
- 30 transfected cell provides a complete response system for investigation or assay of the activity of Y2 receptors with ligands as described above. Transfection systems are useful as living cell cultures for competitive binding assays between known or candidate drugs and
- 35 ligands which bind to the receptor and which are labeled by radioactive, spectroscopic or other reagents. Membrane preparations containing the receptor isolated

from transfected cells are also useful for Y2 receptor activity and competitive binding assays. Functional assays of signal transduction pathways in transfection systems determine a ligand's efficacy of activating the
5 receptor. A transfection system constitutes a "drug discovery system" useful for the identification of natural or synthetic compounds with potential for drug development that can be further modified or used directly as therapeutic compounds to activate or inhibit the
10 natural functions of the Y2 receptor. The transfection system is also useful for determining the affinity and efficacy of known drugs at the Y2 receptor sites.

This invention provides a pharmaceutical composition
15 comprising an effective amount of the Y2 receptor agonist determined by the methods described above and a pharmaceutically acceptable carrier. As used herein, the term "pharmaceutically acceptable carrier" encompasses any of the standard pharmaceutical carriers, such as a
20 phosphate buffered saline solution, water, and emulsions, such as an oil/water or water/oil emulsion, and various types of wetting agents. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. In a further
25 embodiment, the Y2 receptor agonist is not previously known.

This invention further provides a pharmaceutical composition comprising an effective amount of the Y2
30 receptor antagonist determined by the methods described above and a pharmaceutically acceptable carrier. In one embodiment the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. In a further embodiment, the Y2 receptor antagonist is
35 not previously known.

This invention also provides a method of screening drugs

to identify drugs which specifically bind to a Y2 receptor on the surface of a cell which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs
5 under conditions permitting binding of drugs to the Y2 receptor, and determining those drugs which bind specifically to the cell, thereby identifying drugs which specifically bind to a Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another
10 embodiment, the Y2 receptor is a rat Y2 receptor.

This invention also provides a method of screening drugs to identify drugs which specifically bind to a Y2 receptor on the surface of a cell which comprises
15 preparing a cell extract from the cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction with a plurality of drugs under conditions permitting binding of drugs to the
20 Y2 receptor, and determining those drugs which bind specifically to the transfected cell, thereby identifying drugs which bind specifically to a Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

25 This invention also provides a method of screening drugs to identify drugs which act as Y2 receptor agonists which comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with a
30 plurality of drugs under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which activate such Y2 receptor, using a bioassay, such as a second messenger assay, thereby identifying drugs which act as Y2 receptor
35 agonists. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment the Y2 receptor is a rat Y2 receptor. In a further embodiment, the Y2

receptor agonist is not previously known.

This invention provides a method of screening drugs to identify drugs which act as agonists of a Y2 receptor
5 which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding a Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction with a plurality of drugs under conditions permitting the
10 activation of a functional Y2 receptor response, and determining those drugs which activate such receptor, using a bioassay, such as a second messenger assay, thereby identifying drugs which act as Y2 receptor agonists. In one embodiment, the Y2 receptor is a human
15 Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. In a further embodiment, the Y2 receptor agonist is not previously known.

This invention also provides a method of screening drugs
20 to identify drugs which as Y2 receptor antagonists which comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with a plurality of drugs in the presence of a known Y2 receptor agonist such as NPY under conditions permitting the
25 activation of a functional Y2 receptor response, and determining those drugs which inhibit the activation of the receptor, using a bioassay, such as a second messenger assay, thereby identifying drugs which act as Y2 receptor antagonists. In one embodiment, the Y2
30 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. In a further embodiment, the Y2 receptor antagonist is not previously known.

35 This invention provides a method of screening drugs to identify drugs which act as Y2 receptor antagonists which comprises preparing a cell extract from cells transfected

- with and expressing nucleic acid encoding a Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction with a plurality of drugs in the presence of a known Y2 receptor agonist, such as NPY, under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which inhibit the activation of the receptor using a bioassay, such as a second messenger assay, thereby identifying drugs which act as Y2 receptor antagonists. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. In a further embodiment, the Y2 receptor antagonist is not previously known.
- In one embodiment of the above described methods, the second messenger assay comprises measurement of intracellular cAMP. In another embodiment, the second messenger assay comprises measurement of intracellular calcium mobilization.
- The nucleic acid in the cells of the methods described above may have a coding sequence substantially the same as the coding sequences shown in Figures 1, 8 and 9. Preferably, the mammalian cell is nonneuronal in origin.
- An example of a nonneuronal mammalian cell is an COS-7 cell. Other examples of a non-neuronal mammalian cell to be used for functional assays are 293 human embryonic kidney cells, mouse embryonic fibroblast NIH-3T3 cells and LM(tk-) cells. Drug candidates are identified by choosing chemical compounds which bind with high affinity to the expressed Y2 receptor protein in transfected cells, using radioligand binding methods well known in the art, examples of which are shown in the binding assays described herein. Drug candidates are also screened for selectivity by identifying compounds which bind with high affinity to the Y2 receptor but do not bind with high affinity to any other NPY receptor subtype

or to any other known receptor site. Because selective, high affinity compounds interact primarily with the target Y2 receptor site after administration to the patient, the chances of producing a drug with unwanted side effects are minimized by this approach.

This invention provides a pharmaceutical composition comprising an effective amount of a drug identified by the methods described above and a pharmaceutically acceptable carrier.

As used herein, an "effective amount" is an amount of the drug effective to produce the desired result in a subject when administered in accordance with the chosen regimen. Once the candidate drug has been shown to be adequately bio-available following a particular route of administration, for example orally or by injection (adequate therapeutic concentrations must be maintained at the site of action for an adequate period to gain the desired therapeutic benefit), and has been shown to be non-toxic and therapeutically effective in appropriate disease models, the drug may be administered to patients by that route of administration determined to make the drug bio-available, in an appropriate solid or solution formulation, to gain the desired therapeutic benefit.

This invention also provides a method of treating an abnormality in a subject, wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering to a subject an effective amount of the pharmaceutical composition described above, thereby treating the abnormality. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

As used herein, the term "effective amount" means that amount of a drug which is able to produce the desired

result in a subject when administered in accordance with the chosen regimen. Typically, an effective amount is an amount from about 0.01 mg per subject per day to about 500 mg per subject per day. More typically this amount
5 is an amount from about 0.1 mg per subject per day to about 60 mg per subject per day. Most typically, this amount is an amount from about 1 mg per subject per day to about 20 mg per subject per day. Optimal dosages to be administered may be determined by those skilled in the
10 art, and will vary with the particular drug in use, the strength of the preparation, the mode of administration, and the advancement of the disease condition. Additional factors depending on the particular subject being treated will result in a need to adjust dosages, including
15 subject age, weight, gender, diet, and time of administration.

This invention provides a method of treating an abnormality in a subject wherein the abnormality is
20 alleviated by activation of a Y2 receptor which comprises administering to a subject an effective amount of a Y2 receptor agonist determined by the methods described above, thereby treating the abnormality. In one embodiment, the Y2 receptor is a human Y2 receptor. In
25 another embodiment, the Y2 receptor is a rat Y2 receptor.

This invention further provides a method of treating an abnormality in a subject, wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor
30 which comprises administering to a subject an effective amount of the pharmaceutical composition described above, thereby treating the abnormality. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

35 This invention also provides a method of treating an abnormality in a subject, wherein the abnormality is

alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an effective amount of a Y2 receptor antagonist determined by the methods described above, thereby treating the abnormality. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.

This invention provides a nucleic acid probe comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a unique sequence included within the sequence of a nucleic acid molecule encoding a Y2 receptor, for example with a coding sequence included within the sequences shown in Figures 1, 8 and 9. As used herein, the phrase "specifically hybridizing" means the ability of a nucleic acid molecule to recognize a nucleic acid sequence complementary to its own and to form double-helical segments through hydrogen bonding between complementary base pairs. As used herein, a "unique sequence" is a sequence specific to only the nucleic acid molecules encoding the Y2 receptor. In one embodiment the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. Nucleic acid probe technology is well known to those skilled in the art who will readily appreciate that such probes may vary greatly in length and may be labeled with a detectable label, such as a radioisotope or fluorescent dye, to facilitate detection of the probe. Detection of nucleic acid encoding Y2 receptors is useful as a diagnostic test for any disease process in which levels of expression of the corresponding Y2 receptor is altered. DNA probe molecules are produced by insertion of a DNA molecule which encodes Y2 receptor or fragments thereof into suitable vectors, such as plasmids or bacteriophages, followed by insertion into suitable bacterial host cells and replication and harvesting of the DNA probes, all

using methods well known in the art. For example, the DNA may be extracted from a cell lysate using phenol and ethanol, digested with restriction enzymes corresponding to the insertion sites of the DNA into the vector (discussed above), electrophoresed, and cut out of the resulting gel. Examples of such DNA molecules are shown in Figures 1, 8 and 9. The probes are useful for 'in situ' hybridization or in order to locate tissues which express this gene family, or for other hybridization assays for the presence of these genes or their mRNA in various biological tissues. In addition, synthesized oligonucleotides (produced by a DNA synthesizer) complementary to the sequence of a DNA molecule which encodes a Y2 receptor are useful as probes for these genes, for their associated mRNA, or for the isolation of related genes by homology screening of genomic or cDNA libraries, or by the use of amplification techniques such as the Polymerase Chain Reaction. Synthesized oligonucleotides as described may also be used to determine the cellular localization of the mRNA produced by the Y2 gene by in situ hybridization.

This invention also provides a method of detecting expression of a Y2 receptor by detecting the presence of mRNA coding for a Y2 receptor which comprises obtaining total mRNA from the cell using methods well known in the art and contacting the mRNA so obtained with a nucleic acid probe comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a sequence included within the sequence of a nucleic acid molecule encoding the Y2 receptor under hybridizing conditions, and detecting the presence of mRNA hybridized to the probe, thereby detecting the expression of the Y2 receptor by the cell. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. Hybridization of probes to target nucleic acid molecules such as mRNA molecules

employs techniques well known in the art. In one possible means of performing this method, nucleic acids are extracted by precipitation from lysed cells and the mRNA is isolated from the extract using a column which binds the poly-A tails of the mRNA molecules. The mRNA is then exposed to radioactively labelled probe on a nitrocellulose membrane, and the probe hybridizes to and thereby labels complementary mRNA sequences. Binding may be detected by autoradiography or scintillation counting. However, other methods for performing these steps are well known to those skilled in the art, and the discussion above is merely an example.

This invention provides an antisense oligonucleotide having a sequence capable of specifically hybridizing to an mRNA molecule which encodes a Y2 receptor so as to prevent translation of the mRNA molecule. The antisense oligonucleotide may have a sequence capable of specifically hybridizing with the cDNA molecule whose sequence is shown in Figure 1, or with the genomic DNA molecule whose sequences are shown in Figures 8 and 9. A particular example of an antisense oligonucleotide is an antisense oligonucleotide comprising chemical analogues of nucleotides.

This invention also provides a pharmaceutical composition comprising an amount of the oligonucleotide described above effective to decrease activity of a Y2 receptor by passing through a cell membrane and specifically hybridizing with mRNA encoding a Y2 receptor in the cell so as to prevent its translation and a pharmaceutically acceptable carrier capable of passing through a cell membrane. The oligonucleotide may be coupled to a substance which inactivates mRNA, such as a ribozyme. The pharmaceutically acceptable carrier capable of passing through cell membranes may also comprise a structure which binds to a receptor specific for a

selected cell type and is thereby taken up by cells of the selected cell type. The structure may be part of a protein known to bind a cell-type specific receptor, for example an insulin molecule, which would target
5 pancreatic cells. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. DNA molecules having coding sequences substantially the same as the coding sequences shown in Figures 1, 8 and 9 may be used as the
10 oligonucleotides of the pharmaceutical composition.

This invention also provides a method of treating an abnormality in a subject wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor
15 which comprises administering to the subject an effective amount of the pharmaceutical composition described above, thereby treating the abnormality. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor.
20 Several examples of such abnormalities are hypertension, gastrointestinal disorders, epilepsy, sleep disorders, and cognitive disorders, (58-80).

Antisense oligonucleotide drugs inhibit translation of
25 mRNA encoding these receptors. Synthetic oligonucleotides, or other antisense chemical structures are designed to bind to mRNA encoding the Y2 receptor and inhibit translation of mRNA and are useful as drugs to inhibit expression of Y2 receptor genes in patients.
30 This invention provides a means to therapeutically alter levels of expression of Y2 receptors by the use of a synthetic antisense oligonucleotide drug (SAOD) which inhibits translation of mRNA encoding these receptors. Synthetic oligonucleotides, or other antisense chemical
35 structures designed to recognize and selectively bind to mRNA, are constructed to be complementary to portions of the nucleotide sequences shown in Figures 1, 8, and 9 of

DNA, RNA or of chemically modified, artificial nucleic acids. The SAOD is designed to be stable in the blood stream for administration to patients by injection, or in laboratory cell culture conditions, for administration to
5 cells removed from the patient. The SAOD is designed to be capable of passing through cell membranes in order to enter the cytoplasm of the cell by virtue of physical and chemical properties of the SAOD which render it capable of passing through cell membranes (e.g. by designing
10 small, hydrophobic SAOD chemical structures) or by virtue of specific transport systems in the cell which recognize and transport the SAOD into the cell. In addition, the SAOD can be designed for administration only to certain selected cell populations by targeting the SAOD to be
15 recognized by specific cellular uptake mechanisms which binds and takes up the SAOD only within certain selected cell populations. For example, the SAOD may be designed to bind to a receptor found only in a certain cell type, as discussed above. The SAOD is also designed to
20 recognize and selectively bind to the target mRNA sequence, which may correspond to a sequence contained within the sequences shown in Figures 1, 8, and 9 by virtue of complementary base pairing to the mRNA. Finally, the SAOD is designed to inactivate the target
25 mRNA sequence by any of three mechanisms: 1) by binding to the target mRNA and thus inducing degradation of the mRNA by intrinsic cellular mechanisms such as RNase I digestion, 2) by inhibiting translation of the mRNA target by interfering with the binding of translation-
30 regulating factors or of ribosomes, or 3) by inclusion of other chemical structures, such as ribozyme sequences or reactive chemical groups, which either degrade or chemically modify the target mRNA. Synthetic antisense oligonucleotide drugs have been shown to be capable of
35 the properties described above when directed against mRNA targets (74,75). In addition, coupling of ribozymes to antisense oligonucleotides is a promising strategy for

inactivating target mRNA (76). An SAOD serves as an effective therapeutic agent if it is designed to be administered to a patient by injection, or if the patient's target cells are removed, treated with the SAOD
5 in the laboratory, and replaced in the patient. In this manner, an SAOD serves as a therapy to reduce receptor expression in particular target cells of a patient, in any clinical condition which may benefit from reduced expression of Y2 receptors.

10

This invention provides an antibody directed to a Y2 receptor, for example, a monoclonal antibody directed to an epitope of a Y2 receptor present on the surface of a cell and having an amino acid sequence substantially the
15 same as an amino acid sequence for a cell surface epitope of the Y2 receptor included in the amino acid sequences shown in Figures 2, 8 and 9 (Seq. I.D. Nos. 2, 4, and 6, respectively). In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2
20 receptor is a rat Y2 receptor. Amino acid sequences may be analyzed by methods well known in the art to determine whether they produce hydrophobic or hydrophilic regions in the proteins which they build. In the case of cell membrane proteins, hydrophobic regions are well known to
25 form the part of the protein that is inserted into the lipid bilayer which forms the cell membrane, while hydrophilic regions are located on the cell surface, in an aqueous environment. Therefore antibodies to the hydrophilic amino acid sequences shown in Figures 2, 8,
30 and 9 will probably bind to a surface epitope of a Y2 receptor, as described. Antibodies directed to Y2 receptors may be serum-derived or monoclonal and are prepared using methods well known in the art. For example, monoclonal antibodies are prepared using
35 hybridoma technology by fusing antibody producing B cells from immunized animals with myeloma cells and selecting the resulting hybridoma cell line producing the desired

38.

antibody. Cells such as COS-7 cells, LM(tk-) cells, NIH-3T3 cells or 293 human embryonic cells comprising DNA encoding the Y2 receptor and thereby expressing the Y2 receptor may be used as immunogens to raise such an antibody. Alternatively, synthetic peptides may be prepared using commercially available machines and the amino acid sequences shown in Figures 2, 8, and 9 (Seq. I.D. Nos. 2, 4, and 6, respectively). As a still further alternative, DNA, such as a cDNA or a fragment thereof, may be cloned and expressed and the resulting polypeptide recovered and used as an immunogen. These antibodies are useful to detect the presence of Y2 receptors encoded by the isolated DNA, or to inhibit the function of the receptors in living animals, in humans, or in biological tissues or fluids isolated from animals or humans.

This invention provides a pharmaceutical composition which comprises an amount of an antibody directed to a Y2 receptor effective to block binding of ligands to the Y2 receptor, and a pharmaceutically acceptable carrier. A monoclonal antibody directed to an epitope of a Y2 receptor present on the surface of a cell and having an amino acid sequence substantially the same as an amino acid sequence for a cell surface epitope of the Y2 receptor included in the amino acid sequences shown in Figures 2, 8 and 9 are useful for this purpose.

This invention also provides a method of treating an abnormality in a subject, wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an amount of the pharmaceutical composition described above effective to block binding of ligands to the Y2 receptor, thereby treating the abnormality. In a one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. Binding of the antibody to the receptor prevents the receptor from

functioning, thereby neutralizing the effects of activity of the receptor. The monoclonal antibodies described above are both useful for this purpose. Some examples of such abnormalities are hypertension, gastrointestinal disorders, epilepsy, sleep disorders, and cognitive disorders (58-72).

This invention provides a method of detecting the presence of a Y2 receptor on the surface of a cell which comprises contacting the cell with an antibody directed to the Y2 receptor, under conditions permitting binding of the antibody to the receptor, and detecting the presence of the antibody bound to the cell, thereby detecting the presence of a Y2 receptor on the surface of the cell. Such a method is useful for determining whether a given cell is defective in expression of Y2 receptors on the surface of the cell. Bound antibodies are detected by methods well known in the art, for example by binding fluorescent markers to the antibodies and examining the cell sample under a fluorescence microscope to detect fluorescence on a cell indicative of antibody binding. The monoclonal antibodies described above are useful for this purpose.

This invention provides a transgenic nonhuman mammal expressing nucleic acid encoding a Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. This invention also provides a transgenic nonhuman mammal comprising a homologous recombination knockout of the native Y2 receptor. This invention also provides a transgenic nonhuman mammal whose genome comprises antisense nucleic acid complementary to nucleic acid encoding a Y2 receptor so placed as to be transcribed into antisense mRNA which is complementary to mRNA encoding a Y2 receptor and which hybridizes to mRNA encoding a Y2 receptor thereby reducing its translation.

The nucleic acid may additionally comprise an inducible promoter or additionally comprise tissue specific regulatory elements, so that expression can be induced, or restricted to specific cell types. Examples of
5 nucleic acid are DNA or cDNA molecules having a coding sequence substantially the same as the coding sequences shown in Figures 1, 8, and 9. An example of a transgenic animal is a transgenic mouse. Examples of tissue specificity-determining regions are the metallothionein
10 promoter (77) and the L7 promoter (78).

Animal model systems which elucidate the physiological and behavioral roles of Y2 receptors are produced by creating transgenic animals in which the activity of a Y2
15 receptor is either increased or decreased, or the amino acid sequence of the expressed Y2 receptor protein is altered, by a variety of techniques. Examples of these techniques include: 1) Insertion of normal or mutant versions of nucleic acid encoding a Y2 receptor or
20 homologous animal versions of these genes, by microinjection, retroviral infection or other means well known to those skilled in the art, into appropriate fertilized embryos in order to produce a transgenic animal (79). 2) Homologous recombination (80, 81) of
25 mutant or normal, human or animal versions of these genes with the native gene locus in transgenic animals to alter the regulation of expression or the structure of these Y2 receptors. The technique of homologous recombination is well known in the art. It replaces the native gene with
30 the inserted gene and so is useful for producing an animal that cannot express native receptor but does express, for example, an inserted mutant receptor, which has replaced the native receptor in the animal's genome by recombination, resulting in underexpression of the
35 receptor. Microinjection adds genes to the genome, but does not remove them, and so is useful for producing an animal which expresses its own and added receptors,

resulting in overexpression of the receptor. One means available for producing a transgenic animal, with a mouse as an example, is as follows: Female mice are mated, and the resulting fertilized eggs are dissected out of their oviducts. The eggs are stored in an appropriate medium such as M2 medium (79). DNA or cDNA encoding a Y2 receptor is purified from a vector (such as plasmid pcEXV-hY2, pcEXV-rY2a or pcEXV-rY2b described above) by methods well known in the art. Inducible promoters may be fused with the coding region of the nucleic acid to provide an experimental means to regulate expression of the trans-gene. Alternatively, or in addition, tissue specific regulatory elements may be fused with the coding region to permit tissue-specific expression of the trans-gene. The nucleic acid, in an appropriately buffered solution, is put into a microinjection needle (which may be made from capillary tubing using a pipet puller) and the egg to be injected is put in a depression slide. The needle is inserted into the pronucleus of the egg, and the nucleic acid solution is injected. The injected egg is then transferred into the oviduct of a pseudopregnant mouse (a mouse stimulated by the appropriate hormones to maintain pregnancy but which is not actually pregnant), where it proceeds to the uterus, implants, and develops to term. As noted above, microinjection is not the only method for inserting nucleic acid into the egg cell, and is used here only for exemplary purposes.

Since the normal action of receptor-specific drugs is to activate or to inhibit the receptor, the transgenic animal model systems described above are useful for testing the biological activity of drugs directed against these Y2 receptors even before such drugs become available. These animal model systems are useful for predicting or evaluating possible therapeutic applications of drugs which activate or inhibit these Y2 receptors by inducing or inhibiting expression of the

native or trans-gene and thus increasing or decreasing activity of normal or mutant Y2 receptors in the living animal. Thus, a model system is produced in which the biological activity of drugs directed against these Y2
5 receptors are evaluated before such drugs become available. The transgenic animals which over or under produce the Y2 receptor indicate by their physiological state whether over or under production of the Y2 receptor is therapeutically useful. It is therefore useful to
10 evaluate drug action based on the transgenic model system. One use is based on the fact that it is well known in the art that a drug such as an antidepressant acts by blocking neurotransmitter uptake, and thereby increases the amount of neurotransmitter in the synaptic
15 cleft. The physiological result of this action is to stimulate the production of less receptor by the affected cells, leading eventually to decreased activity. Therefore, an animal which has decreased receptor activity is useful as a test system to investigate
20 whether the actions of such drugs which result in decreased activity are in fact therapeutic. Another use is that if increased activity is found to lead to abnormalities, then a drug which down-regulates or acts as an antagonist to a Y2 receptor is indicated as worth
25 developing, and if a promising therapeutic application is uncovered by these animal model systems, activation or inhibition of the Y2 receptor is achieved therapeutically either by producing agonist or antagonist drugs directed against these Y2 receptors or by any method which
30 increases or decreases the activity of these Y2 receptors in humans or other mammals.

This invention provides a method of determining the physiological effects of expressing varying levels of Y2
35 receptors which comprises producing a transgenic nonhuman animal whose levels of Y2 receptor expression are varied by use of an inducible promoter which regulates Y2

receptor expression. This invention also provides a method of determining the physiological effects of expressing varying levels of Y2 receptors which comprises producing a panel of transgenic nonhuman animals each
5 expressing a different amount of Y2 receptor. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. Such animals may be produced by introducing different amounts of nucleic acid encoding a Y2 receptor into the
10 oocytes from which the transgenic animals are developed.

This invention also provides a method for identifying a Y2 receptor antagonist capable of alleviating an abnormality in a subject, wherein the abnormality is
15 alleviated by decreasing the activity of a Y2 receptor which comprises administering the antagonist to a transgenic nonhuman mammal described above and determining whether the antagonist alleviates the physical and behavioral abnormalities displayed by the
20 transgenic nonhuman mammal as a result of the activity of a Y2 receptor, thereby identifying a Y2 antagonist. In one embodiment, the Y2 receptor is a human Y2 receptor, In another embodiment, the Y2 receptor is a rat Y2 receptor. This invention further provides an antagonist
25 identified by the method described above. Examples of nucleic acid molecules are DNA or cDNA molecules having a coding sequence substantially the same as the coding sequences shown in Figures 1, 8, and 9.

30 This invention provides a pharmaceutical composition comprising an amount of the antagonist described supra effective to alleviate an abnormality wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor and a pharmaceutically acceptable carrier.

35 This invention further provides a method for treating an abnormality in a subject wherein the abnormality is

alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an effective amount of the pharmaceutical composition described above, thereby treating the abnormality.

5

This invention provides a method for identifying a Y2 receptor agonist capable of alleviating an abnormality wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering the agonist to
10 the transgenic nonhuman mammal described above and determining whether the agonist alleviates the physical and behavioral abnormalities displayed by the transgenic nonhuman mammal, thereby identifying a Y2 receptor agonist. In one embodiment, the Y2 receptor is a human
15 Y2 receptor. In another embodiment, the Y2 receptor is a rat Y2 receptor. This invention further provides an agonist identified by the method described above.

This invention also provides a pharmaceutical composition
20 comprising an effective amount of a Y2 receptor agonist identified by the method described above and a pharmaceutically acceptable carrier.

This invention further provides a method for treating an
25 abnormality in a subject wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering to the subject an effective amount of the pharmaceutical composition described above, thereby treating the abnormality.

30

This invention provides a method for diagnosing a predisposition to a disorder associated with the expression of a specific Y2 receptor allele which comprises: a) obtaining nucleic acid of subjects
35 suffering from the disorder; b) performing a restriction digest of the nucleic acid with a panel of restriction enzymes; c) electrophoretically separating the resulting

nucleic acid fragments on a sizing gel; d) contacting the resulting gel with a nucleic acid probe capable of specifically hybridizing to nucleic acid encoding a Y2 receptor and labelled with a detectable marker; e) 5 detecting labelled bands which have hybridized to the nucleic acid encoding a Y2 receptor labelled with a detectable marker to create a unique band pattern specific to the nucleic acid of subjects suffering from the disorder; f) preparing nucleic acid obtained for 10 diagnosis by steps a-e; and g) comparing the unique band pattern specific to the nucleic acid of subjects suffering from the disorder from step e and the nucleic acid obtained for diagnosis from step f to determine whether the patterns are the same or different and 15 thereby to diagnose predisposition to the disorder if the patterns are the same. This method may also be used to diagnose a disorder associated with the expression of a specific Y2 receptor allele. In one embodiment, the Y2 receptor is a human Y2 receptor. In another embodiment, 20 the Y2 receptor is a rat Y2 receptor.

This invention provides a method of preparing the isolated, purified Y2 receptor which comprises a) constructing a vector adapted for expression in a cell 25 which comprises the regulatory elements necessary for the expression of nucleic acid in the cell operatively linked to the nucleic acid encoding a Y2 receptor as to permit expression thereof, wherein the cell is selected from the group consisting of bacterial cells, yeast cells, insect 30 cells and mammalian cells; b) inserting the vector of step (a) in a suitable host cell; c) incubating the cells of step (b) under conditions allowing the expression of a Y2 receptor; d) recovering the receptor so produced; and e) purifying the receptor so recovered. An example 35 of an isolated Y2 receptor is an isolated protein having substantially the same amino acid sequence as the amino acid sequences shown in Figures 2, 8 and 9. For

example, cells can be induced to express receptors by exposure to substances such as hormones. The cells can then be homogenized and the receptor isolated from the homogenate using an affinity column comprising, for example, PVY or NPY or another substance which is known to bind to the receptor. The resulting fractions can then be purified by contacting them with an ion exchange column, and determining which fraction contains receptor activity or binds anti-receptor antibodies.

10

The above described method for preparing a Y2 receptor uses recombinant DNA technology methods well known in the art. For example, isolated nucleic acid encoding Y2 receptor is inserted in a suitable vector, such as an expression vector. A suitable host cell, such as a bacterial cell, or a eukaryotic cell such as a yeast cell, is transfected with the vector. Y2 receptor is isolated from the culture medium by affinity purification or by chromatography or by other methods well known in the art.

20

This invention identifies for the first time a new receptor protein, its amino acid sequence, its human gene and its rat homologue. Furthermore, this invention describes a previously unrecognized group of receptors within the definition of a Y2 receptor. The information and experimental tools provided by this discovery are useful to generate new therapeutic agents, and new therapeutic or diagnostic assays for this new receptor protein, its associated mRNA molecule or its associated genomic DNA. The information and experimental tools provided by this discovery will be useful to generate new therapeutic agents, and new therapeutic or diagnostic assays for this new receptor protein, its associated mRNA molecule, or its associated genomic DNA.

30

35

Specifically, this invention relates to the first

isolation of a human genomic clone encoding a Y2 receptor. A new human gene for the receptor identified herein as Y2 has been identified and characterized. In addition, the human Y2 receptor has been expressed in 293
5 human embryonic kidney cells. The pharmacological binding properties of the protein encoded have been determined, and these binding properties classify this protein as a novel human NPY/PYY receptor which we designate as a human Y2 receptor. Mammalian cell lines
10 expressing this human Y2 receptor at the cell surface have been constructed, thus establishing the first well-defined, cultured cell lines with which to study this Y2 receptor.

15 This invention will be better understood by reference to the Experimental Details which follow, but those skilled in the art will readily appreciate that the specific experiments detailed are only illustrative of the invention as described more fully in the claims which
20 follow thereafter.

EXPERIMENTAL DETAILS**cDNA Cloning**

Total RNA was prepared by a modification of the guanidine thiocyanate method (13), from 6 grams of human hippocampus. Poly A⁺RNA was purified with a FastTrack kit (Invitrogen Corp., San Diego, CA). Double stranded (ds) cDNA was synthesized from 4 µg of poly A⁺ RNA according to Gubler and Hoffman (14), except that ligase was omitted in the second strand cDNA synthesis. The resulting DS cDNA was ligated to BstXI/EcoRI adaptors (Invitrogen Corp.), the excess of adaptors was removed by chromatography on Sephacryl 500 HR (Pharmacia-LKB) and the ds-cDNA size selected by chromatography on Sephacryl 1000 (Pharmacia-LKB). High molecular weight fractions were ligated in pcEXV.BS (An Okayama and Berg expression vector) cut by BstXI as described by Aruffo and Seed (15). The ligated DNA was electroporated in E. coli MC 1061 (Gene Pulser, Biorad). A total of 2.2×10^6 independent clones with an insert mean size of 3 kb could be generated. The library was plated on Petri dishes (Ampicillin selection) in pools of 0.4 to 1.2×10^4 independent clones. After 18 hours amplification, the bacteria from each pool were scraped, resuspended in 4 mL of LB media and 1.5 mL processed for plasmid purification by the alkali method (16). 1 mL aliquots of each bacterial pool were stored at -85°C in 20% glycerol.

Isolation of a cDNA clone encoding a human hippocampal Y2 receptor.

DNA from pools of ≈ 5000 independent clones was transfected into COS-7 cells by a modification of the DEAE-dextran procedure (17). COS-7 cells were grown in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% fetal calf serum, 100 U/mL of penicillin, 100 µg/mL of streptomycin, 2mM L-glutamine (DMEM-C) at 37°C in 5% CO₂. The cells were seeded one day before transfection at

a density of 30,000 cells/cm² in 6 well plates (Becton Dickinson, Lincoln Park, NJ). On the next day, cells were washed twice with Phosphate Buffer Saline (PBS), 400 µl of transfection cocktail was added containing 1/10 of the DNA from each pool and DEAE-dextran (500 µg/mL) in PBS. After a 30 min. incubation at 37°C, 1.6 mL of chloroquine (80 µM in DMEM-C) was added and the cells incubated a further 2.5 hours at 37°C. The media was aspirated from each well and 1 mL of 10% DMSO in DMEM-C added. After 2.5 min. incubation at room temperature, the media was aspirated, each well washed once with 1 mL PBS and the cells incubated 24 hours in DMEM-C. The cells were then trypsinized and seeded on Lab-Tek chamber slides (1 chamber, Permaxox slide from Nunc Inc., Naperville, IL), incubated in 2 ml DMEM-C for another 24 hours and the binding assay was performed on the slides.

After two washes with PBS, positive pools were identified by incubating the cells with 1 nM (3x10⁶ cpm per slide) of porcine [¹²⁵I]-PYY (New England Nuclear; specific activity=2200Ci/mmol) in 20 mM Hepes-NaOH pH 7.4, CaCl₂ 1.26 mM, MgSO₄ .81 mM, KH₂PO₄ .44 mM, KCl 5.4, NaCl 10mM, .1% bovine serum albumin, .1% bacitracin for 1 hour at room temperature. After six washes (five seconds each) in binding buffer without ligand, the monolayers were fixed in 2.5% glutaraldehyde in PBS for five minutes, washed twice two minutes in PBS, dehydrated in ethanol baths for two minutes each (70, 80, 95, 100%) and air dried.

The slides were then dipped in 100% photoemulsion (Kodak type NTB2) at 42°C and exposed in the dark for 48 hours at 4°C in light proof boxes containing drierite. Slides were developed for three minutes in Kodak D19 developer (32 g/l of water), rinsed in water, fixed in Kodak fixer for 5 minutes, rinsed in water, air dried and mounted with Aqua-Mount (Lerner Laboratories, Pittsburgh, PA).

Slides were screened at 25x total magnification.

A single clone, CG-13, was isolated by sib selection as described (18). DS-DNA was sequenced with a Sequenase
5 kit (US Biochemical, Cleveland, OH) according to the manufacturer. Nucleotide and peptide sequences analysis were performed with GCG programs (Genetics Computer group, Madison, WI).

10 Northern Blot

A multiple tissue Northern blot (MTN blot, Contech, Palo Alto, CA) carrying mRNA purified from various human brain areas was hybridized at high stringency according to the manufacturer's specifications. The probe was a 1.15 kb
15 DNA fragment corresponding to the entire coding region of the human Y2 receptor as shown in Figure 10.

Southern Blot:

A Southern blot (Geno-Blot, Clontech, Palo Alto, CA)
20 containing human genomic DNA cut with five different enzymes (8 µg DNA per lane) was hybridized at high stringency according to the manufacturer's specifications. The probe was a DNA fragment corresponding to the TM1-TM5 coding region of the human
25 Y2 receptor, as shown in Figure 11.

Cloning and Expression of Two Isoforms of the Rat NPY/PYY (Y2) Receptor

To obtain the rat homologue of the human NPY/PYY (Y2)
30 receptor, we designed and synthesized oligonucleotide probes derived from the nucleotide sequences corresponding approximately to the transmembrane (TM) regions of the amino acid sequence of the human Y2 receptor (TM 1 - 7) as shown in Figure 11. The
35 overlapping oligomers used were as follows:

(TM1: nts. #190-257, (+) strand/5'-

CAAGTTGTTCTCATATTGGCCTACTGCTCCATCATCTTGCTTGGGGTAAT-3'
(Seq. I.D. No. 7) and (-) strand/5'-
ATCACCACATGGATCACCAAGGAGTTGCCAATTACCCCAAGCAAGATGAT-3'
(Seq. I.D. No. 8)

5

TM2: nts. #301-370, (+) strand/5'-
TTTTTCATTGCCAATCTGGCTGTGGCAGATCTTTTGGTGAACACT-3' (Seq.
I.D. No. 9) and (-) strand/5'-
AGGTAAGAGTGAACGGTAGACACAGAGTGTTACCCAAAAGATCTG-3' (Seq.
10 I.D. No. 10).

TM3: nts. #411-480, (+) strand/5'-
CCACCTGGTGCCCTATGCCCAGGGCCTGGCAGTACAAGTATCCAC-3' (Seq.
I.D. No. 11) and (-) strand/5'-
15 CAGGGCAATTACTGTCAAGGTGATTGTGGATACTTGTACTGCCAG-3' (Seq. I.
D. No. 12).

TM4: nts. #531-600, (+) strand/5'-
AATCAGCTTCCTGATTATTGGCTTGGCCTGGGGCATCAGTGCCCT-3' (Seq.
20 I.D. No. 13) and (-) strand/5'-
GAAGATGGCCAGGGGACTTGCCAGCAGGGCACTGATGCCCCAGGC-3' (Seq.
I.D. No. 14)

25 **TM5:** nts. #691-760, (+) strand/5'-
ACTGTCTATAGTCTTTCTTCCTTGTGTGATCTTGTATGTTTTGCCT-3' (Seq.
I.D. No. 15) and (-) strand/5'-
TGTAGGAAAATGATATAATGCCAGAGGCCAAACATACAAGATCA-3' (Seq.
I.D. NO. 16)

30 TM6: nts. #850-919, (+) strand/5'-
CTGGTGTGTGTGGTGGTGGTGTGTTGCGGTCAGCTGGCTGCCTCTC-3' (Seq.
I.D. No. 17) and (-) strand/5'-
TGTC AACGGCAAGCTGGAAGGCATGGAGAGGCAGCCAGCTGACCG-3' (Seq.
I.D. No. 18)

35

TM7: NTS. #955-1028, (+) strand/5'-
CTCATCTTTCACAGTGTTCACATCATCGCCATGTGCTCCACTTTTGC-3' (Seq.

I.D. No. 19) and (-) strand/5'-
TTCATCCAGCCATAGAGAAGGGGATTGGCAAAAGTGGAGCACATGGC-3' (Seq.
I.D. No. 20).

- 5 The probes were labeled with [³²P]-ATP and [³²p]-CTP by synthesis with the large fragment of DNA polymerase.

Hybridization was performed at 40°C in a solution containing 25% formamide, 10% dextran sulfate, 5X SSC (1X SSC is 0.15 M sodium chloride, 0.015 M sodium citrate), 1X Denhardt's (0.02% polyvinylpyrrolidone, 0.02% Ficoll, and 0.02% bovine serum albumin), and 100 µg/ml of sonicated salmon sperm DNA. The filters were washed at 40°C in 0.1X SSC containing 0.1% sodium dodecyl sulfate (SDS) and exposed at -70°C to Kodak XAR film in the presence of one intensifying screen. Lambda phage hybridizing to the probes were plaque purified by successive plating and rescreening. A genomic clone hybridizing with six out of seven TM probes, designated rs5a, was isolated using this method. A 4.0 kb EcoRI fragment of rs5a was subcloned into the eukaryotic expression vector EXJ.RH modified from pcEXV-3 (73) for sequence analysis and expression studies. The nucleotide sequence of the fragment in EXJ.RH was analyzed on both strands by the Sanger dideoxy nucleotide chain-termination method (82) using Sequenase (U.S. Biochemical Corp., Cleveland, Ohio).

A second genomic clone, termed rs26a, was also isolated using the hybridization conditions described above and exhibited the same hybridization profile with TM probes. In contrast with rs5a, however, rs26a contained an internal EcoRI restriction enzyme site not present in the other clone. To further investigate potential differences between the two clones, a 3.9 kb SalI/KpnI fragment of rs26a was subcloned into the expression vector EXJ.HR for sequence analysis and expression studies. The nucleotide sequence of the fragment was analyzed on both strands by the Sanger dideoxy nucleotide chain-termination method as described above.

35 Cell Culture

COS-7 cells were grown on 150 mm plates in Dulbecco's Modified Eagle Medium (DMEM) with supplements (10% bovine

calf serum, 4 mM glutamine, 100 units/ml penicillin/100 μ g/ml streptomycin) at 37 °C, 5% CO₂. Stock plates of COS-7 cells were trypsinized and split 1:6 every 3-4 days.

- 5 Human embryonic kidney cells 293 cells were grown on 150 mm plates in Dulbecco's Modified Eagle Medium (DMEM) with supplements (10% bovine calf serum, 4 mM glutamine, 100 units/ml penicillin/100 μ g/ml streptomycin) at 37 °C, 5% CO₂. Stock plates of 293 cells were trypsinized and split
10 1:6 every 3-4 days.

- Mouse embryonic fibroblast NIH-3T3 cells were grown on 150 mm plates in Dulbecco's Modified Eagle Medium (DMEM) with supplements (10% bovine calf serum, 4 mM glutamine,
15 100 units/ml penicillin/100 μ g/ml streptomycin) at 37 °C, 5% CO₂. Stock plates of NIH-3T3 cells were trypsinized and split 1:15 every 3-4 days.

- SK-N-Be(2) human neuroblastoma cells were grown similarly
20 in 225 cm² flasks using 50% Eagle's Modified Essential Media, 50% Ham's Nutrient Mixture F-12, 15% fetal bovine serum, 2 mM glutamine, 100 units/ml penicillin/80 units/ml streptomycin, and 1% non-essential amino acids. Stock flasks of SK-N-Be(2) cells were trypsinized and
25 split 1:10 every 7 days.

DNA Transfection for Pharmacological Characterization

- All cloned receptor subtypes studied (human Y1, human Y2, human Y4, rat Y2a and rat Y2b) were transiently
30 transfected into COS-7 cells by the DEAE-dextran method, using 1 μ g of DNA/10⁶ cells (17). The cDNA corresponding to the cloned Y4 receptor was disclosed in U.S. patent application 08/176,412 filed on December 28, 1993, currently pending.

35

Membrane Preparation

Membranes were harvested from COS-7 cells 48 hours after

transfection and from SK-N-Be(2) seven days after splitting. Adherent cells were washed twice in ice-cold phosphate buffered saline (138 mM NaCl, 8.1 mM Na₂HPO₄, 2.5 mM KCl, 1.2 mM KH₂PO₄, 0.9 mM CaCl₂, 0.5 mM MgCl₂, pH 7.4) and lysed by sonication in ice-cold hypotonic buffer (20 mM Tris-HCl, 5 mM EDTA, pH 7.7). Large particles and debris were cleared by low speed centrifugation (200 x g, 20 min, 4 °C). Membranes were collected from the supernatant fraction by high speed centrifugation (32,000 x g, 18 min, 4 °C), washed with ice-cold hypotonic buffer, and collected again by high speed centrifugation (32,000 x g, 18 min, 4 °C). The final membrane pellet was resuspended by sonication into a small volume (~500 µl) of ice-cold binding buffer (10 mM NaCl, 20 mM HEPES, 0.22 mM KH₂PO₄, 1.26 mM CaCl₂, 0.81 mM MgSO₄, pH 7.4). Protein concentration was measured by the Bradford method (19) using Bio-Rad Reagent, with bovine serum albumin as a standard.

20 Radioligand Binding to Membrane Suspensions

Membrane suspensions were diluted in binding buffer supplemented with 0.1% bovine serum albumin and 0.1% bacitracin to yield membrane protein concentrations of ~ 0.02 mg/ml for human Y1 receptors, ~ 0.003 mg/ml for CG-13 receptors, and ~ 0.25 mg/ml for SK-N-Be(2) (under these assay conditions, non-specific binding of ¹²⁵I-PYY to membranes was less than 10%). ¹²⁵I-PYY and non-labeled peptide competitors were also diluted to desired concentrations in supplemented binding buffer. Individual samples were then prepared in 96-well polypropylene microliter plates by mixing membrane suspensions (200 µl), ¹²⁵I-PYY (25 µl), and non-labeled peptides or supplemented binding buffer (25 µl). Samples were incubated in a 30 °C water bath with constant shaking for 120 min. Incubations were terminated by filtration over Whatman GF/C filters (pre-coated with 0.5% polyethyleneimine and air-dried before

use). Filter-trapped membranes were counted for ^{125}I in a gamma counter. Non-specific binding was defined by 100 nM human NPY. Specific binding in time course and competition studies was typically 80%; most non-specific binding was associated with the filter. Binding data were analyzed using nonlinear regression and statistical techniques available in the GraphPAD InPlot package (San Diego, CA).

10 Creation Of A Stably Expressing Cell Line

pcEXV-hY2 DNA was transfected into the 293 human embryonic kidney cell line by the calcium phosphate transfection method. The 293 cells were grown in minimal essential medium (MEM) with Hank's salts, plus 2 mM glutamine, 100 international units of penicillin, streptomycin at 100 ug/ml, and 10% fetal calf serum, in 5% CO_2 at 37°C. Stably transfected cells were selected for two weeks in media containing G-418 (1 mg/ml) and screened for the ability to bind ^{125}I -PYY. Several clones were selected based on preliminary measurements of cell density. One positive clone, designated 293-hY2-10, was chosen for further characterization in binding and functional assays. This clone displayed saturable binding of ^{125}I -porcine PYY in membrane preparations: B_{max} = 880 fmol/mg membrane protein, K_d = 3 pM, (n=3). When incubated with various concentrations of human PYY, it elicited a concentration-dependent inhibition of forskolin-stimulated cAMP accumulation as determined by radioimmunoassay. Clone 293-hY2-10 also elicited a concentration-dependent increase in free intracellular calcium as determined by Fura-2 fluorescence. The calcium response, which probably reflects mobilization of intracellular calcium stores, was inhibited by pretreatment of cells with pertussis toxin. EC_{50} values for both the cAMP and the calcium response are currently under investigation.

pcEXV-hY2 DNA was also transfected into the mouse embryonic NIH-3T3 cell line using the methods described above to create another cell line stably expressing human Y2 receptors. A clone designated N-hY2-5 was selected and characterized as above.

Tissue Localization and Gene Expression: Reverse Transcriptase PCR

Human tissues obtained from National Disease Research Interchange were homogenized and total RNA extracted using guanidine isothiocyanate/CsCl cushion method. RNA was treated with DNase to remove any contaminating genomic DNA. cDNA was prepared from total RNA with random hexanucleotide primers using the reverse transcriptase Superscript II (BRL, Gaithersburg, MD). An aliquot of the first strand cDNA (250ng of total RNA) was amplified in a 50 μ l PCR reaction mixture (200 μ M dNTPs final concentration) containing 1.2U of Taq polymerase in the buffer supplied by the manufacturer (Perkin-Elmer Corporation), and 1 μ M of primers, using a program consisting of 30 cycles of 94°C./2', 68°C./2', and 72°C./3', with a pre- and post-incubation of 95°C./5' and 72°C./10', respectively. PCR primers for human Y2 were designed against the human Y2 sequence in the third intracellular loop and carboxyl terminal regions: 5'-GGGAGTATTCGCTGATTGAGATCAT-3' (SEQ. I.D. No. 21) and 5'-GCCTTGAATGTACGGACACCTC-3' (SEQ. I.D. No. 22), respectively.

The PCR products were run on a 1.5% agarose gel and transferred to charged nylon membranes (Zetaprobe GT, BioRad), and analyzed as Southern blots. Hybridization probes corresponding to the receptor region flanked by PCR primers were prepared (5'-CTGATGGTAGTGGTCATTTGCAGCTCCAGGACTGACATGGTTCTT-3') (SEQ. I.D. No. 23) and pre-screened for the absence of cross-reactivity with human Y1 and Y4 receptor subtypes.

Filters were hybridized with the phosphorylated probes and washed under high stringency. Labeled PCR products were visualized on X-ray film. Similar PCR and Southern blot analyses were conducted with primers and probe
5 directed to the housekeeping gene, glyceraldehyde-3-phosphate dehydrogenase (Clontech, Palo Alto, CA), and demonstrated that equal amounts of cDNA from the different tissues were being assayed for Y2 receptor expression.

10

Localization of NPY Y2 messenger RNA in the rat central nervous system

The distribution of NPY Y2 mRNA in the rat brain was determined using *in situ* hybridization histochemistry.
15 Male Sprague-Dawley rats were euthanized with CO₂, decapitated and the brains rapidly removed and frozen in isopentane. Coronal sections were cut at 11 μ m on a cryostat and thaw-mounted onto poly-L-lysine coated slides and stored at -80° C until use. Prior to
20 hybridization, tissues were fixed in 4% paraformaldehyde, treated with 5 mM dithiothreitol, acetylated in 0.1 M triethanolamine containing 0.25% acetic anhydride, delipidated with chloroform, and dehydrated in graded ethanols.

25

The oligonucleotide probes employed to characterize the distribution of the NPY Y2 mRNA were synthesized using a Cyclone Plus DNA synthesizer (Milligen/Bioscience) and gel-purified. The probes used and their sequences are
30 given in Table 7. Probe specificity was established by performing the *in situ* hybridization protocol described below on cells transfected with the rat NPY Y2 DNA (supra), or on nontransfected control cells. In addition, both sense and antisense probes were employed
35 on cells and rat tissues.

Probes were 3'-end labeled with ³⁵S-dATP (1200 Ci/mmol,

New England Nuclear, Boston, MA) to a specific activity of 10^9 dpm/ μ g using terminal deoxynucleotidyl transferase (Boehringer Mannheim; Indianapolis, IN). The radiolabeled probes were purified on Biospin 6 chromatography columns (Bio-Rad; Richmond, CA), and diluted in hybridization buffer to a concentration of 1.5×10^6 cpm/ μ l. The hybridization buffer consisted of 50% formamide, 4X sodium citrate buffer (1X SSC = 0.15 M NaCl and 0.015 M sodium citrate), 1X Denhardt's solution (0.2% polyvinylpyrrolidone, 0.2% Ficoll, 0.2% bovine serum albumin), 50 mM dithiothreitol, 0.5 mg/ml salmon sperm DNA, 0.5 mg/ml yeast tRNA, and 10% dextran sulfate. One hundred μ l of the diluted probe was applied to each section, which was then covered with a Parafilm coverslip. Hybridization was carried out overnight in humid chambers at 40 to 55°C. The following day the sections were washed in two changes of 2X SSC for one hour at room temperature, in 0.1X SSC for 30 min at 50-60°C, and finally in 0.1X SSC for 30 min at room temperature. Tissues were dehydrated in graded ethanols and apposed to Kodak XAR-5 film for 3 days to 6 weeks at -20°C, then dipped in Kodak NTB3 autoradiography emulsion diluted 1:1 with 0.2% glycerol water. After exposure at 4°C for 2 to 8 weeks, the slides were developed in Kodak D-19 developer, fixed, and counterstained with hematoxylin and eosin.

Functional Assay: Radioimmunoassay of cAMP

Stably transfected cells were seeded into 96-well microliter plates and cultured until confluent. To reduce the potential for receptor desensitization, the serum component of the media was reduced to 1.5% for 4 to 16 hours before the assay. Cells were washed in Hank's buffered saline, or HBS (150 mM NaCl, 20 mM HEPES, 1 mM CaCl_2 , 5 mM KCl, 1 mM MgCl_2 , and 10 mM glucose) supplemented with 0.1% bovine serum albumin plus 5 mM theophylline and pre-equilibrated in the same solution

for 20 min at 37 °C in 5% CO₂. Cells were then incubated 5 min with 10 µM forskolin and various concentrations of receptor-selective ligands. The assay was terminated by the removal of HBS and acidification of the cells with
5 100 mM HCl. Intracellular cAMP was extracted and quantified with a modified version of a magnetic bead-based radioimmunoassay (Advanced Magnetics, Cambridge, MA). The final antigen/antibody complex was separated from free ¹²⁵I-cAMP by vacuum filtration through a PVDF
10 filter in a microliter plate (Millipore, Bedford, MA). Filters were punched and counted for ¹²⁵I in a Packard gamma counter. Binding data were analyzed using nonlinear regression and statistical techniques available in the GraphPAD Prism package (San Diego, CA).

15

Functional Assay: Intracellular Calcium Mobilization

The intracellular free calcium concentration was measured by microspectrofluorometry using the fluorescent indicator dye Fura-2/AM. Stably transfected cells were
20 seeded onto a 35 mm culture dish containing a glass coverslip insert. Cells were washed with HBS and then loaded with 100 µl of Fura-2/AM (10 µM) for 20 to 40 min. After washing with HBS to remove the Fura-2/AM solution, cells were equilibrated in HBS for 10 to 20 min. Cells
25 were then visualized under the 40X objective of a Leitz Fluovert FS microscope and fluorescence emission was determined at 510 nm with excitation wave lengths alternating between 340 nm and 380 nm. Raw fluorescence data were converted to calcium concentrations using
30 standard calcium concentration curves and software analysis techniques.

Reagents

Cell culture media and supplements were from Specialty
35 Media (Lavallette, NJ). Cell culture plates (150 mm) were from Corning (Corning, NY). Cell culture flasks (225 cm²) and polypropylene microliter plates were from

Co-star (Cambridge, MA). Porcine ^{125}I -PYY was from New England Nuclear (Boston, MA). NPY and related peptide analogs were from either Bachem California (Torrance, CA) or Peninsula (Belmont, CA). Whatman GF/C filters were
5 Brandel (Gaithersburg, MD). Bio-Rad Reagent was from Bio-Rad (Hercules, CA). Bovine serum albumin and bacitracin were from Sigma (St. Louis, MO). All other materials were reagent grade.

RESULTS**Isolation of a cDNA clone encoding a human hippocampal Y2 receptor**

5 In order to clone a human NPY receptor subtype (Y2), we
used an expression cloning strategy in COS-7 cells (20,
21, 22). This strategy was chosen for its extreme
sensitivity since it allows detection of a single
"receptor positive" cell by direct microscopic
10 autoradiography.

Since the Y2 receptor is described as a presynaptic
receptor, it is difficult to locate cell bodies that
actually contain this specific mRNA in restricted brain
15 areas. We reasoned that human hippocampus was a good
source of mRNA since it contains both a large number of
interneurons and has been shown to carry a particularly
dense population of Y2 receptors (23, 24, 25, 26). A
human hippocampal cDNA library of 2.2×10^6 independent
20 recombinants with a 3 kb average insert size was
fractionated into 440 pools of ≈ 5000 independent clones.
From the first 200 pools tested, three gave rise to
positive cells in the screening assay (#145, 158 and
189). The last 220 pools tested were all negative.

25 Since both Y1 and Y2 receptor subtypes are expressed in
the hippocampus (2), we analyzed the DNA of positive
pools by PCR with Y1 specific primers. Pools #145 and
#158 turned out to contain cDNAs encoding an Y1 receptor,
30 but pool #189, negative by PCR (data not shown), likely
contained a cDNA encoding a human hippocampal NPY
receptor that was not Y1. Pool #189 was subdivided in 20
pools of 1000 clones each, and a preliminary
pharmacological characterization was run on COS-7 cells
35 transfected with DNA prepared from the secondary pools.
This preliminary analysis revealed that a 100 fold excess
of cold [Leu³¹-Pro³⁴]NPY totally inhibited binding of ¹²⁵I-

PYY to control COS-7 cells transfected with the Y1 gene. In contrast, no significant inhibition of binding was observed when the same experiment was performed on COS-7 cells transfected with secondary pool #189-17 (data not shown). This is consistent with pool #189 containing a cDNA encoding a human hippocampal Y2 receptor. The sib selection was therefore pursued on pool #189 until a single clone was isolated (designated CG-13).

10 The isolated clone carries a 4.2 kb cDNA. This cDNA contains an open reading frame between nucleotides 1002 and 2147 that encodes a 381 amino acid protein (SEQ. I.D. No. 2). The unusually long 5' untranslated region could be involved in the regulation of translation efficiency or mRNA stability. The flanking sequence around the putative initiation codon conforms to the Kozak consensus sequence for optimal translation initiation (27, 28).

The hydrophobicity plot displayed seven hydrophobic, putative membrane spanning regions which makes the human hippocampal Y2 receptor a member of the G-protein coupled superfamily. The nucleotide and deduced amino acid sequences are shown in Figure 1 and Figure 2, respectively.

25 Like most G-protein coupled receptors, the Y2 receptor contains a consensus sequence for N-linked glycosylation, in the amino terminus (position 11) involved in the proper expression of membrane proteins (29). The Y2 receptor carries two highly conserved cysteine residues in the first two extracellular loops that are believed to form a disulfide bond stabilizing the functional protein structure (30). The Y2 receptor shows 7 potential phosphorylation sites for protein kinase C in positions 11, 27, 64, 145, 188, 250 and 340, 2 casein kinase sites in positions 174 and 358, and 2 cAMP- and cGMP-dependent protein kinase phosphorylation sites in positions 146 and

350. It should be noted that 7 of those 11 potential phosphorylation sites are located in intra-cellular loops 1, 2 and 3 as well as in the carboxyl terminus of the receptor and therefore could play a role in regulating functional characteristics of the Y2 receptor (30). A potential palmitoylation site is present in the sequence at the cysteine found in position 326. A large number of G-protein coupled receptors carry a cysteine in the same position and O'Dowd et al. have speculated that it plays an important role in the functional coupling of the human β_2 -adrenergic receptor (31). The formation of this additional cytosolic loop may influence the mobility of the receptor across the membrane (32).

When compared to the published human Y1 cDNA clone (10, 11) the Y2 sequence shows surprisingly low homology both at the nucleotide level, 48.1% (Figure 3) and overall amino acid level, 31% (Figure 4). The transmembrane domain identity of the human hippocampal Y2 receptor with other 7 TM receptors is shown in Table 1. The low TM identity with other G-protein coupled receptor families, with other peptide receptors and especially with the Y1 subtype raises the possibility that Y2 receptor subtypes belong to a new distinct sub-family of 7 TM peptide receptors. Conversely, NPY receptor subtypes could form a sub-family where members show unusually low levels of overall homology. Applicants have also cloned the human Y4 receptor, and this receptor also exhibits a low degree of homology with the human Y2 receptor (Table 1). It is interesting to observe that the mouse orphan receptor MUSGIR (mouse glucocorticoid induced receptor, 33) shows the highest TM identity (42%, Table 1) with our human Y2 receptor. The same comparison between human Y1 (or Y4) and Y2 TM regions only gives a score of 41% identity. If we were comparing the human Y2 receptor sequence with the human homolog of the MUSGIR receptor, the level of identity might even be higher. Therefore the MUSGIR

receptor could be related to the NPY receptors and bind members of the pancreatic polypeptide ligand family. A full pharmacological evaluation of the human GIR homolog with NPY, PYY and PP related ligands is now underway to
5 verify this hypothesis.

Using the human Y2 probe, northern hybridizations reveal a unique band at 4.3 kb in human brain after a three-day exposure (Figure 16). This is in good agreement with the
10 4.2 kb cDNA that we isolated by expression cloning and indicates that our cDNA clone is full-length. The mRNA encoding the human Y2 receptor is present in significant amounts in amygdala, corpus callosum, hippocampus, and subthalamic nucleus. A faint band is detectable in
15 caudate nucleus, hypothalamus and substantia nigra. No signal could be detected in thalamus. It should be noted that Clontech's MTN blot does not carry any mRNA from cortex or brain stem.

20 Southern hybridizations to human genomic DNA followed by high stringency washes (Figure 17) suggest that the human genome contains a single Y2 receptor gene (single band with EcoRI, HindIII, BamHI and PstI). The faint bands at 9 and 12 kb observed with BglII can be explained by the
25 presence of two BglII restriction sites in the coding region of the human Y2 sequence and are also consistent with a single Y2 receptor gene.

30 Pharmacology of the transiently expressed human Y2 receptor

The Y2-like pharmacology of CG-13, originally identified by whole cell autoradiographic techniques, was further defined by membrane binding assays. The gene for the human hippocampal Y2 receptor was transiently expressed
35 in COS-7 cells for full pharmacological evaluation. ¹²⁵I-PYY bound specifically to membranes from COS-7 cells transiently transfected with the CG-13 construct. The

time course of specific binding was measured in the presence of 0.06 nM ^{125}I -PYY (Figure 5). The association curve was biphasic, with approximately 55% of the specific binding occurring during an initial rapid phase and 45% following a slower time course. For the rapid phase, the observed association constant (K_{obs}) was $1.28 \pm 0.02 \text{ min}^{-1}$ and $t_{1/2}$ was 0.5 min; equilibrium binding was 95% complete within 2 min and 100% complete within 5 min ($n = 3$). For the slow phase, K_{obs} was $0.02 \pm 0.00 \text{ min}^{-1}$ and $t_{1/2}$ was 37 min; equilibrium binding was 90% complete within 120 min, 95% complete within 160 min and 100% complete within 280 min ($n = 3$). Total equilibrium binding, composed of both phases, was 95% complete within 120 min and 100% complete within 240 min. The biphasic association curve may reflect a complex pattern of receptor surface binding followed by access to deep-seated binding sites, as has been suggested by Schwartz and co-workers for Y2 receptors (34). For comparison, we also measured the time course of binding to human Y1 receptors transiently expressed in COS-7 cells (Figure 5). The association curve was monophasic, with a K_{obs} of $0.06 \pm 0.02 \text{ min}^{-1}$ and a $t_{1/2}$ of 12 min; equilibrium binding was 95% complete within 51 min and 100% complete within 90 min ($n = 3$). The different patterns of association for CG-13 and human Y1 receptors suggest novel mechanisms of receptor/ligand interaction.

Saturation binding data for ^{125}I -PYY were fit to a one-site model with an apparent K_d of $0.069 \pm 0.009 \text{ nM}$ and an apparent B_{max} of $7.8 \pm 0.4 \text{ pmol/mg}$ membrane protein, corresponding to approximately 7.5×10^5 receptors/cell ($n = 3$; Figure 6). Given that the transfection efficiency was 20-30% (data not shown), the receptor density on transfected cells was probably closer to 3×10^6 /cell. Membranes from mock-transfected cells, when prepared and analyzed in the same way as those from CG-13-transfected cells, displayed no specific binding of

¹²⁵I-PYY. We conclude that the ¹²⁵I-PYY binding sites observed under the described conditions were derived from the CG-13 construct.

5 Y2 receptor recognition is thought to depend primarily upon the four C-terminal residues of NPY (Arg³³- Gln³⁴- Arg³⁵- Tyr³⁶-NH₂) preceded by an amphipathic α -helix (M4, M5); exchange of Gln³⁴ with Pro³⁴ is not well tolerated (4, 5). We therefore chose several C-terminal fragments and
10 C-terminal modified peptides for competition binding studies. The rank order of affinity for selected compounds was derived from competitive displacement of ¹²⁵I-PYY (Fig. 7 and Table 3). The CG-13 receptor was compared with two model systems: 1) the cloned human Y1
15 receptor (10, 11) transiently expressed in COS-7 cells, and 2) the Y2-like receptor population expressed by human SK-N-BE(2) neuroblastoma cells (2, 8). To our knowledge, no models for human Y3 and human PP receptors have been described.

20

CG-13 bound with high affinity to human NPY (K_i = 0.69 nM) and even more so to human PYY (K_i = 0.39 nM). The K_i values are in agreement with numerous reports of pharmacologically defined Y2 receptors studied in NPY
25 binding and functional assays (2). The opposite rank order was observed with human Y1 receptors, combined with stronger receptor/binding interactions (K_i = 0.049 and 0.085 nM for human NPY and human PYY, respectively). It is interesting in this regard that CG-13 bound ¹²⁵I-PYY (K_d
30 = 0.069 nM) with higher affinity than PYY (K_i = 0.39 nM), suggesting that iodination may stabilize the receptor/ligand complex. The human Y1 receptor, in contrast, bound both ¹²⁵I-PYY (K_d = 0.062 + 0.010 nM, n = 3, data not shown) and PYY (K_i = 0.085 nM) with comparable
35 affinity. The fact that CG-13 and the human Y1 receptor bound NPY, PYY and ¹²⁵I-PYY with different magnitudes and rank orders of affinity most likely reflects distinct

mechanisms of peptide recognition which could potentially be exploited for the development of subtype-selective non-peptide ligands.

5 CG-13 also bound with high affinity to porcine NPY ($K_i = 0.86$ nM), which differs from human NPY by containing Leu¹⁷ in the PP-fold rather than Met¹⁷. CG-13 was relatively insensitive to N-terminal deletion of NPY and PYY; the affinity for porcine NPY₂₂₋₃₆ was only 5-fold less than
10 that for full length porcine NPY. Extreme deletion of α -helical structure was less well tolerated; the affinity for porcine NPY₂₆₋₃₆ was 240-fold less than that for full length porcine NPY. Human [Leu³¹,Pro³⁴]NPY and human PP, both having Pro³⁴ rather than Glu³⁴, did not bind well (K_i
15 > 300 nM). Hydrolysis of the carboxyl terminal amide to free carboxylic acid, as in NPY free acid, also disrupted binding affinity for CG-13 ($K_i > 300$ nM). The terminal amide appears to be a common structural requirement for pancreatic polypeptide family/receptor interactions.

20 The competitive displacement data indicate that CG-13 binds PYY with equal or greater affinity than NPY. The C-terminal region of NPY is the primary pharmacophore. CG-13 does not tolerate exchange of Gln³⁴ with Pro³⁴, as
25 revealed by low affinity interactions with human [Leu³¹,Pro³⁴]NPY and human PP. The binding profile, which is shared by SK-N-BE(2) cell receptors but not by human Y1 receptors, is characteristic of the pharmacologically defined Y2 receptor (refs. 2, 8; see also Table 2). The
30 membrane binding studies therefore confirm and extend our assessment that CG-13 encodes a human Y2 receptor.

The pharmacological profile of the human Y2 receptor was further investigated using peptide analogs related to
35 NPY, PYY, and PP (Table 4). CG-13 did not discriminate human and frog analogs of NPY ($K_i = 0.74$ and 0.87 nM, respectively), human and porcine analogs of NPY₂₋₃₆ ($K_i =$

2.0 and 1.2 nM, respectively), human and porcine analogs of [Leu³¹, Pro³⁴]NPY (K_i > 130 and > 540 nM, respectively), or human NPY and human [Tyr-O-Me²¹]NPY (K_i = 0.74 and 1.6 nM, respectively). This last derivative was tested based on the proposal that it was selective for central vs. peripheral NPY receptors, with high binding affinity in rat CNS but low potency in rat vas deferens relative to NPY (83). For the receptors under investigation, however, [Tyr-O-Me²¹]NPY and human NPY yielded highly similar binding profiles. The NPY derivative with greatest selectivity for CG-13 was C2-NPY, a C² to C²⁷ disulfide-stabilized derivative of NPY with an 8-amino-octanoic linker replacing NPY₅₋₂₄ (K_i = 3.5 nM, \geq 20-fold selective for CG-13 over Y1 and Y4 receptors). C2-NPY has been described as a Y2-selective compound (3).

Three additional PYY derivatives yielded distinctive binding profiles. CG-13 bound with highest affinity and greatest selectivity to human PYY₃₋₃₆ (K_i = 0.70 nM, \geq 20-fold selective for CG-13 over Y1 and Y4 receptors). PYY₃₋₃₆ is a major form of PYY-like immunoreactivity in blood and could therefore mediate CG-13-dependent processes in vivo (84, 85). Porcine PYY was relatively nonselective and similar in binding affinity to human PYY (K_i = 0.35 nM and 0.36 nM, respectively). Human [Pro³⁴]PYY was lacking in binding affinity for CG-13 (K_i > 310), further supporting the argument that Pro³⁴ is disruptive for high affinity peptide binding to the CG-13 receptor.

Six additional PP derivatives were investigated. Those peptides which resemble human PP in that they contain Pro³⁴ (bovine, rat, avian, and frog PP) displayed no activity in the CG-13 binding assay. High affinity binding was detected only for salmon PP (K_i = 0.17 nM), which is distinguished by containing Gln³⁴. When the C-terminus of human PP was modified to more closely

resemble human NPY, as in [Ile³¹, Gln³⁴]PP, the binding affinity for CG-13 was increased dramatically ($K_i = 20$ nM). It has been reported previously that [Ile³¹, Gln³⁴]PP was more active than PP in Y2 binding assays, while
5 exhibiting decreased potency for putative PP receptors in rat vas deferens (86).

Several proposed NPY antagonists were analyzed for their ability to bind to CG-13 receptors. These include PYX-1
10 and PYX-2, C-terminal derivatives of NPY reported to antagonize NPY-mediated feeding and neurotransmitter release (87, 88, 89). Neither synthetic peptide bound to CG-13 with high affinity or selectivity ($K_i = 684$ for PYX-1 and $K_i > 1000$ nM for PYX-2). [D-Trp³²]NPY is an NPY
15 derivative reported to regulate feeding behavior when injected into the hypothalamus of rats (90); this analog was inactive in the CG-13 binding assay. Another inactive compound was NPY₁₋₂₄ amide, a peptide reported to antagonize NPY in the rat vas deferens (83).

20

Human tissue Y2 receptor macrolocalization: PCR

Human Y2 mRNA was detected by PCR techniques in a broad range of human tissues (Table 5). Relatively intense hybridization signals were detected in total brain,
25 thoracic artery, coronary artery, and penis, with more moderate levels in frontal brain, ventricle, mesentery, stomach and ileum. Relatively low levels were detected in nasal mucosa and pancreas. Several other tissues were negative for Y2 mRNA as measured by this technique,
30 including atrium, liver, and uterus.

Cloning and Expression of Two Isoforms of the Rat NPY/PYY (Y2) Receptor

Two rat genomic clones homologous to the human Y2
35 receptor were isolated, termed rs5a (Figure 8) and rs26a (Figure 9). The nucleotide sequence of rs5a is 86.5% identical in the coding region to that of the human Y2

receptor (Figure 10), and can encode a 381 amino acid protein with 94.5% identity to the human Y2 amino acid sequence (Figure 11). In the putative transmembrane domains (TMs), the protein predicted by rs5a exhibits
5 98.2% amino acid identity with the human Y2 receptor (Figure 11). This high degree of primary sequence identity is often observed for species homologues, and strongly suggests that the receptor encoded by rs5a is the rat Y2 receptor. However, even a single amino acid
10 substitution can influence the functional properties of a receptor; thus, even species homologues exhibiting a high level of sequence identity may display different pharmacological properties (*infra*), underscoring the importance of obtaining both rat and human receptors for
15 use in drug development.

Sequence analysis of the second genomic clone revealed that rs26a also encoded a full-length rat Y2 receptor; however, rs26a contains two nucleotide changes when
20 compared with the sequence of rs5a. Both nucleotide changes result in amino acid substitutions in the predicted rat Y2 receptor protein. With two (2) amino acid changes, the protein encoded by rs26a is 99.7% identical to that of rs5a. Compared with the human Y2
25 receptor, the nucleotide sequence identity of rs26a is 85.2% and the amino acid sequence identity is 98.2%. This clone therefore encodes an isoform of the rat Y2 receptor distinct from that encoded by rs5a. The locations of the amino acid substitutions (N-terminus and
30 5/6 loop; see Figure 3) suggest that they could potentially influence receptor function. The Y2 receptors encoded by rs5a and rs26a are likely to represent allelic variants at the same gene locus; however, rs26a could represent a second rat Y2 gene.
35 Accordingly, we have designated the isoform encoded by rs5a as the rat Y2a receptor, and designated the isoform encoded by rs26a as the rat Y2b receptor.

The primary sequences of rat and human Y2 receptors, while highly related, show distinct patterns of sequence motifs for N-linked glycosylation, N-myristoylation, and protein phosphorylation. For example, the rat Y2a differs from the rat Y2b in that it contains an additional site for phosphorylation by protein kinase C. Further, the human Y2 differs from both rat Y2 isoforms in containing two additional sites for N-linked glycosylation, two additional sites for cAMP- and cGMP-dependent protein phosphorylation, an additional site for casein kinase II phosphorylation, one additional site for protein kinase C phosphorylation, and two fewer sites for N-myristoylation. These sites could mediate differences in the function or regulation of the three receptors. The isolation of two rat homologues of the Y2 receptor provides the means to compare the pharmacological properties of the rat and human Y2 receptors (see below) in relation to their observed differences in primary structures. These data will be critical to the design and testing of human therapeutic agents acting at these sites.

Binding Studies with Rat Y2 Homologs

The DNA corresponding to the rat Y2a homolog was transiently expressed in COS-7 cells for membrane binding studies. The binding of ^{125}I -PYY to the rat Y2a receptor was saturable over a radioligand concentration of 0.5 pM to 2.5 nM. Binding data were fit to a one-site model with an apparent $K_d = 0.26$ nM and a receptor density of 5100 fmol/mg membrane protein. As determined by using peptide analogs within the pancreatic polypeptide family, the rat Y2a pharmacological profile resembles that for the human Y2 receptor (Table 6). Each receptor analog is relatively tolerant of N-terminal ligand deletion (the human apparently more so than the rat) and intolerant of any peptide containing Pro³⁴ or a modified C-terminus (as

in NPY free acid or [D-Trp³²]NPY).

The rat Y2b clone, which differs from rat Y2a by two amino acid changes one in the N-terminal tail (from Leu²⁰ to Phe²⁰) and another in the third intracellular loop (from Thr²⁶⁶ to Met²⁶⁶), has been subjected only to a preliminary investigation. Membranes from COS-7 cells transiently transfected with the rat Y2b receptor were incubated with 0.08 nM ¹²⁵I-PYY and analyzed for specific binding after incubation at 30 °C for 120 min. Membranes from transfected cells bound 310 fmol ¹²⁵I-PYY/ mg membrane protein, whereas membranes from mock-transfected cells (receiving vector without receptor cDNA insert) bound only 3 fmol ¹²⁵I-PYY/ mg membrane protein. It remains to be determined whether there exist any pharmacological or functional differences between the ratY2a and rat Y2b receptors.

Localization of NPY Y2 messenger RNA in the rat central nervous system

In control experiments, hybridization signals for rat NPY Y2 mRNA were seen only with the antisense probes (probe sequences shown in Table 7), and only over cells which had been transfected with the rat Y2 DNA (Figure 18). The probes were designed to recognize both rat Y2a and rat Y2b. Neither mock transfected cells nor cells transfected with rat NPY Y1 mRNA exhibited hybridization signals. On rat brain sections, no hybridization signals were obtained with the sense probes, only with the antisense probes.

The distribution of NPY Y2 mRNA observed in coronal sections through the rostrocaudal extent of rat brain is shown in Figure 12 and Table 8. Hybridization signals were seen over many areas of the rat brain (Figure 12), which, at the microscopic level, were confined to the cytoplasm of neuronal profiles (data not shown). In the

telencephalon, the most intense hybridization signals were observed over the CA3 region of the hippocampus (Figure 12B-E) and over the anteroventral aspect of the medial nucleus of the amygdala (Figure 12C, D). Less
5 intense signals were found over the olfactory tubercle, the lateral septal nucleus (Figure 12A), and over the basomedial nucleus and posteromedial cortical nucleus of the amygdala (Figure 12D, E). Scattered neurons with hybridization signal were also seen in the central
10 amygdaloid nucleus. In cortex, silver grains were seen over large neurons in the piriform region.

Among diencephalic structures, the arcuate nucleus of the hypothalamus exhibited the most intense hybridization
15 signal for NPY Y2 mRNA (Figure 12D, E). In this area, most of the neurons appeared to be labelled, and many neurons were also labelled in the region of the tuber cinereum lateral to the arcuate nucleus. In addition, both the dorsomedial and ventromedial hypothalamic nuclei
20 contained appreciable hybridization signals over subpopulations of neurons (Figure 12C, D). In the dorsal and ventral premammillary nuclei, hybridization signal was seen over many neurons (Figure 12E). In the thalamus, neurons in the centromedial nucleus were
25 labelled (Figure 12C, D), while a smaller, less intensely labelled group of cells was visible in the paraventricular nucleus (Figure 12D).

In the mesencephalon, medulla, and pons, few structures
30 were labelled with the antisense oligonucleotide probe. Those exhibiting a moderate level of hybridization signal were the dorsal and caudal linear raphe (Figure 12F), the pontine nucleus, and the posterior dorsal tegmental nucleus (Figure 12G). In the spinal cord, labelling was
35 observed over scattered large neurons in lamina 9 (Figure 12H). Silver grains were also found over a few large neurons in the dorsal root ganglion.

Receptor/G protein Interactions: Effects of Guanine Nucleotides

For a given G protein-coupled receptor, a portion of the receptor population in a membrane homogenate typically exists in the high affinity ligand binding state as a receptor/G protein complex. The binding of GTP or a non-hydrolyzable analog to the G protein causes a conformational change in the receptor which favors a low affinity ligand/binding state (110). We investigated whether the non-hydrolyzable GTP analog, Gpp(NH)p, would alter the binding of human NPY or ¹²⁵I-PYY to Y2 receptors transiently expressed in COS-7 cells. The competition curve produced by human NPY was evaluated in the absence and presence of 100 μ M Gpp(NH)p. The human Y2 receptor was relatively insensitive to the Gpp(NH)p compared to the rat Y2a receptor (Figure 13). The IC₅₀ for human NPY binding to the human Y2 receptor was increased from 2.2 nM to 3.3 nM; specific binding of ¹²⁵I-PYY was decreased by only 4% (n = 5). The IC₅₀ for human NPY binding to the rat Y2a receptor was altered very little (from 0.7 nM to 1.2 nM, n = 2); specific binding of ¹²⁵I-PYY, however, was decreased by 23% (n = 2). A similar pattern of sensitivity to Gpp(NH)p was reported for ¹²⁵I-PYY binding to rat brain (91). The difference between the rat and human Y2 receptor clones could be explained by several factors, including 1) the types of G proteins available in COS-7 cells, 2) the level of receptor reserve in COS-7 cells (note that human Y2 receptor density was greater than that of the rat Y2a receptor), and 3) the efficiency of receptor/G protein coupling (92; 93).

Stable Expression Systems: Characterization in Binding Assays

Untransfected 293 and NIH-3T3 cells were pre-screened for specific ¹²⁵I-PYY binding and found to be negative (data not shown). After co-transfection with the human Y2 cDNA plus a G-418-resistant gene and selection with G-418,

surviving colonies were screened for specific binding of ^{125}I -PYY. Two positive clones were identified and isolated for further study (293 clone #10 and NIH-3T3 clone #5). The binding of ^{125}I -PYY to membranes from the 293 stable clone was saturable over a radioligand concentration range of 0.5 pM to 2.5 nM. Binding data were fit to a one-site binding model with an apparent K_d of 3 ± 1 pM and a receptor density of 880 ± 50 fmol/mg membrane protein (mean \pm s.e.m., $n = 3$). Membranes from stably transfected NIH-3T3 cells displayed similar binding properties, with an apparent K_d of 8 ± 2 pM and a receptor density of 160 ± 60 fmol/mg membrane protein (mean \pm s.e.m., $n = 2$). Membranes from both stable clones were incubated with 0.08 nM ^{125}I -PYY in the presence or absence of 100 μM Gpp(NH)p. Specific binding of ^{125}I -PYY to Y2 receptors in 293 cell membranes was reduced 32% in the presence of the guanine nucleotide, whereas specific binding to Y2 receptors in NIH-3T3 cell membranes was reduced only 6% under the same conditions. The data serve to emphasize that the receptor/G protein interactions for a given receptor clone can vary depending upon the resident G proteins in the host cell line (93). Additional factors such as receptor density and receptor reserve can also play a role (92).

25

Functional Assay: cAMP

Activation of all Y-type receptors described thus far is thought to involve coupling to G-proteins which are inhibitory for adenylate cyclase activity (G_i or G_o) (1). Based on these prior observations, we investigated the ability of PYY to inhibit forskolin-stimulated cAMP accumulation in 293 cells stably expressing the human Y2 receptor. Incubation of intact cells with 10 μM forskolin produced a 10-fold increase in cAMP accumulation over a 5 minute period, as determined by radioimmunoassay. Simultaneous incubation with human PYY decreased the forskolin-stimulated cAMP accumulation by

35

71% in stably transfected 293 cells (Figure 14) but not in untransfected cells (data not shown). The NPY-mediated response was concentration-dependent ($EC_{50} = 0.25$ nM). We conclude that human Y2 receptor activation can result in decreased cAMP accumulation, very likely through inhibition of adenylate cyclase activity. Similar results were obtained for NIH-3T3 cells stably transfected with the human Y2 receptor, in which human NPY decreased forskolin-stimulated cAMP accumulation by 50% in transfected cells with an EC_{50} of 0.21 nM (Figure 14).

Peptides selected for their ability to bind to the transiently expressed human Y2 receptor were further investigated for functional activity using stably transfected 293 cells (Table 9). All peptides with measurable binding affinity were able to mimic the effects of PYY on cAMP accumulation. EC_{50} values were generally within a 10-fold range of K_i values, often lower in magnitude (Table 9). We also investigated the functional activity of the reported feeding behavior modulator [D-Trp³²]NPY. Consistent with this peptide's low binding affinity for the human Y2 receptor, we detected no functional activity at concentrations up to 0.3 μ M, or when tested at 0.3 μ M for antagonism of the functional response (data not shown). The reported NPY receptor antagonists PYX-1 and PYX-2 were also inactive when tested under the same paradigm.

Functional Assay: Intracellular Calcium Mobilization

The intracellular free calcium concentration was increased in 293 cells stably transfected with the human Y2 receptor after application of 1 μ M human PYY ($\Delta [Ca^{2+}]_i = 80$ nM; Figure 15). The PYY-mediated response was concentration-dependent, with $EC_{50} = 39$ nM, $n = 2$ (Figure 15). PYY-induced calcium mobilization was relatively maintained in the presence of 1 mM extracellular EGTA (Δ

[Ca²⁺]_i = 64 nM for 1 μM human PYV), suggesting that intracellular calcium stores are the primary source of the transient calcium flux. Pretreatment with pertussis toxin (100 ng/ml for 24 hours) decreased the response to 300 nM human PYV by 93%, thereby supporting a G protein-linked signal transduction pathway. Untransfected 293 cells did not respond to human PYV (data not shown). The calcium mobilization assay provides a second pathway through which Y2 receptor activation can be measured.

10

DISCUSSION

Attempts to isolate the NPY Y2 receptor subtype based on sequence homology with the Y1 receptor have not been successful so far. Therefore, we chose an expression cloning approach where a functional receptor is actually detected with exquisite sensitivity on the surface of transfected cells, using a highly specific iodinated ligand. Using this strategy, we have identified a human cDNA encoding the pharmacologically defined Y2 receptor. The fact that we had to screen 2.2 x 10⁶ independent clones with a 3 kb average insert size to find one clone reveals either a very strong bias against Y2 cDNA cloning in the cDNA library construction procedure, or the Y2 mRNA is expressed at very low levels in human hippocampal tissue. The longest reading frame in the cDNA encodes a 381 amino acid protein with an estimated molecular weight of 42 kD. Given the fact that there is an N-linked glycosylation site in the amino terminus, the apparent molecular weight could be slightly higher and in good agreement with published data on the molecular weight of the human hippocampal Y2 receptor at 50 kD (36). The Y2 receptor carries a large number of potential phosphorylation sites which could be involved in the regulation of its functional characteristics.

The nucleotide and amino acid sequence analysis both reveal low identity levels with all 7-TM receptors including the human Y1 and Y4 receptors. The highest transmembrane amino acid identity is found with the mouse
5 MUSGIR receptor. A pharmacological profile on the human GIR homolog will be established with NPY, PYV and pancreatic polypeptide related ligands to find out if this orphan receptor belongs to the same pharmacologically defined neuropeptide Y receptor sub-
10 family. The human Y2 receptor shares very low amino acid identity with the previously cloned human Y1 receptor (31% overall and 41% in transmembrane regions). The human Y2 receptor also displays a unique pharmacological profile and a unique time course of association with ¹²⁵I-
15 PYV. The dramatic differences in sequence and pharmacological profile between the human Y1 and Y2 receptors suggest that they might be encoded by two unrelated genes whose products have evolved into binding the same family of ligands. Conversely, they could have
20 diverged from a common ancestor very early in evolution and undergone multiple mutations leading to distinct pharmacological characteristics.

Northern analysis reveals a 4.3 kb band in human brain
25 and demonstrates that our 4.2 kb Y2 cDNA is full-length. Southern analyses are consistent with the human genome containing a single Y2 receptor gene.

The pharmacological binding profile established in our
30 initial characterization served primarily to establish the CG-13 as a human Y2 receptor. The additional data included here reflect an increased understanding of receptor ligand/interactions. We now know, for example, that C2-NPY and PYV₃₋₃₆ can be used to compete for Y2
35 receptor sites with greater affinity and selectivity than the C-terminal fragments of NPY originally described. We also know that certain peptides which are thought to

antagonize NPY-dependent effects, such as [D-Trp³²]NPY, PYX-1, and PYX-2, are unable to compete for binding of the human Y2 receptor clone described here. Our evidence does not therefore support the cloned Y2 receptor as the
5 molecular target of these particular peptides in vivo or in vitro.

Human Y2 receptor mRNA was detected by PCR techniques in a broad range of human tissues (Table 5). Relatively
10 intense hybridization signals were detected in total brain, thoracic artery, coronary artery, and penis, with more moderate levels in frontal brain, ventricle, and mesentery. This distribution is consistent with evidence for Y2 receptor localization and receptor-dependent
15 effects in CNS, cardiovascular, and reproductive physiology (94). Moderate hybridization signals were also detected in stomach and ileum, consistent with evidence for Y2-mediated effects on chief cell cAMP accumulation (95) and also intestinal electrolyte flux
20 (61; 96). Relatively low levels were detected in nasal mucosa and pancreas, two tissues in which Y2-like receptors have been reported to regulate vasoconstriction and pancreatic secretion, respectively (97, 98, 99). A more definitive localization of the Y2 receptor mRNA and
25 receptor expression (i.e., whether on neurons, enterocytes, vascular smooth muscle cells, etc.) is attainable through *in situ* hybridization and receptor autoradiography techniques.

30 The distribution of NPY Y2 mRNA described here in rat brain has a number of potential implications, and raises a number of important questions. Among these are; 1) how does the distribution of this mRNA correlate with that of NPY itself; 2) how does the Y2 mRNA distribution relate
35 to the putative autoradiographic localization of Y2 receptors described by previous investigators; and 3) what are the functional implications of the Y2 mRNA

distribution?

Correlation with NPY immunoreactivity

Neuropeptide Y is one of the most abundant and widely distributed peptides in the mammalian brain (100). In some areas, NPY Y2 mRNA appears to be co-distributed with NPY-immunoreactive (NPYir) neurons, although colocalization in the same neuron(s) remains to be established. In both the arcuate nucleus of the hypothalamus and the medial nucleus of the amygdala, the distribution of Y2 mRNA overlaps with the distribution of NPYir neurons demonstrated by immunocytochemical studies (100, 101). In addition, both areas contain moderate plexuses of NPYir axons. These observations leave open the question of presynaptic/postsynaptic nature of the Y2 receptor. In most other areas of the brain, the Y2 mRNA does not appear to be co-distributed with NPYir neurons, but instead correlates better with the distribution of NPYir terminal fields, suggesting a postsynaptic localization.

Comparison with receptor autoradiography

A number of investigators have described the distribution of NPY receptors based on the autoradiographic localization of radiolabelled NPY ligands, among them [¹²⁵I]NPY and [¹²⁵I]peptide YY (PYY), in combination with subtype-selective displacers. The Y2 receptor has been localized by combining [¹²⁵I]PYY with the Y2-selective mask NPY₁₃₋₃₆ (94). The results of such studies suggest that the Y2 receptor is widely distributed in rat brain, being most abundant in the hippocampus, olfactory bulb, and hypothalamus. We have seen no NPY Y2 mRNA in the olfactory bulb, but both hippocampus and hypothalamus contain Y2 mRNA. However, the pharmacological characterization of NPY receptor subtypes is incomplete at present, and some of the Y2-like binding may be attributable to the so-called atypical Y1 receptor, or to

other undiscovered NPY receptor subtypes.

Our *in situ* results suggest that the receptor autoradiographic characterization of the Y2 receptor is likely to be accurate for some areas. The projection
5 fields of neurons containing the Y2 mRNA are important in this respect. Thus the pyramidal neurons of the CA3 region of the hippocampus, which contain relatively intense Y2 hybridization signals, project in a topographic fashion to the lateral septum (102), an area
10 which supposedly contains a high proportion of Y2 receptors (103, 23, 94). Similarly, the olfactory bulb appears to contain mainly NPY receptors of the Y2 subtype. While there is no Y2 mRNA in the olfactory bulb, the piriform cortex contains many neurons which are
15 labelled with the Y2 antisense probe, and provides a major source of olfactory bulb afferents. The localization of NPY Y2 mRNA in the arcuate nucleus of the hypothalamus is particularly interesting, as NPYir neurons in this nucleus provide the NPY innervation of
20 much of the hypothalamus, including the paraventricular and dorsomedial nuclei (104, 105). It is unclear at present which receptor subtype(s) predominate in the paraventricular nucleus, but based on our results with the Y2 mRNA, and those of Mikkelsen and colleagues with
25 the Y1 mRNA (106, 107), both Y1 and Y2 should be present. Similar arguments can be pursued for most of the regions which contain Y2 mRNA, however a definitive profile of Y2 receptor localization awaits the introduction of Y2 selective ligands.

30

Functional considerations

Neuropeptide Y is involved in a number of physiological functions, including the regulation of food intake, neuronal excitability, cardiovascular regulation, and
35 circadian rhythms. With regard to food intake, the paraventricular nucleus of the hypothalamus is one site which has been intensively investigated, and has been

demonstrated to be a prominent locus of action for the orexigenic effects of NPY. The localization of NPY Y2 mRNA in the arcuate nucleus, and the projections of the arcuate to the paraventricular nucleus, suggest the involvement of this receptor in feeding.

In the hippocampus, NPY immunoreactivity is found mainly in interneurons which innervate pyramidal cells. Here, NPY has been demonstrated to reduce synaptic excitation in areas CA1 and CA3. This has been assumed to be mediated by a Y2 receptor (108), as C-terminal fragments of NPY are effective in the assay. The localization of Y2 mRNA in pyramidal cells of CA3 indicates that this receptor may be involved in the termination of convulsive activity, such as in epilepsy.

The rat Y2a and Y2b receptor analogs represent essential tools for pharmaceutical drug development. Drug candidates screened primarily against human receptors must also be characterized at the rat (or other relevant species analog) so that data generated from in vivo models can be interpreted accurately. While the current panel of peptides revealed no major differences in pharmacological profile between the human Y2 and rat Y2a receptor analogs, even a single amino acid difference between receptors displaying high sequence similarity could have dramatic effects on ligand binding affinity (109). The rat Y2b receptor represents an additional opportunity to evaluate species-dependent differences in ligand binding. It remains to be determined whether the rat Y2b receptor plays a singular role in rat Y2 receptor pharmacology, due either to unique ligand binding properties or to distinctive localization patterns.

We established functional assays for human Y2 receptor activation in both 293 and NIH-3T3 cells based on receptor-dependent inhibition of forskolin-stimulated

cAMP accumulation (Table 9). The EC_{50} values for peptides in these assays were generally smaller than the corresponding K_i values, suggesting that receptor activation occurs through a high affinity state of the receptor which is not predominantly represented under the conditions of the binding assay. Such a scenario would be consistent with the weak effect of Gpp(NH)p on radioligand binding to the human Y2 receptor in membrane homogenates.

10

Our characterization of the Y2 receptor stably expressed in 293 cells also shows definitively that the Y2 receptor can couple simultaneously to both cAMP regulation and calcium mobilization in a single cell type. The calcium mobilization in 293 cells, at least, appears to occur through a pertussis toxin-sensitive G protein. The EC_{50} for the human PYY-mediated calcium response is significantly larger than that for the cAMP response in the same host cell (39 nM vs. 0.31 nM, respectively), suggesting that calcium mobilization requires promiscuous coupling of the receptor to a G protein other than that involved in cyclase regulation. The exact identities of the G proteins mediating these receptor activation events, whether G_i , G_o , G_z , or another type, remain to be determined.

We now have several Y2 receptor expression systems from which to choose, each uniquely suited to different uses. The transient expression system in COS-7, for example, allows us to generate sufficient quantities of membranes for routine structure/activity relationship measurements. We can also produce mutant receptors by site-directed mutagenesis or related enzymatic techniques and express them transiently in COS-7 for a comparison of pharmacological properties with those of the wild-type receptor. In this way, we can gain insight into receptor binding pockets, ligand binding domains, and mechanisms

of activation. The stable expression system in 293 and NIH-3T3 cells offers the convenience of a single transfection followed by routine passaging techniques. The stable expression system also offers the opportunity to select for optimum receptor expression levels, G protein populations, and signal transduction pathways, all of which are critical elements for in vitro functional assays. Such assays can be used to determine agonist or antagonist activity in receptor-selective compounds, thereby generating critical information for drug design.

The expression cloning of a human Y2 receptor allows, for the first time, the ability to develop NPY-receptor subtype specific drugs and represents a major advance in our ability to analyze NPY-mediated physiological processes. Pharmacologically defined Y2 receptors have a widespread anatomical distribution (2). They represent the predominant NPY receptor in brain, with the highest density in hippocampus and relatively high expression in almost all other areas including olfactory bulb, basal ganglia, amygdaloid complex, thalamic and hypothalamic nuclei, pituitary, pineal gland, cerebellum, and brainstem. This distribution is consistent with northern blot analysis, which shows that the Y2 MRNA is present in amygdala, candate nucleus, corpus callosum, hippocampus, hypothalamus, substantia nigra and subthalamic nucleus.

Peripheral localization includes sympathetic neurons, dorsal root ganglia, stomach chief cells, intestinal enterocytes, kidney proximal tubule, trachea, and vascular smooth muscle. Y2 receptors are therefore in a position to potentially regulate a variety of physiological functions including cognitive enhancement, circadian rhythm, EEG synchronization, body temperature, blood pressure, locomotor activity, neuroendocrine release, sympathetic activation, sensory transmission, gastrointestinal function, intestinal secretion, renal

absorption, and cardiovascular function (1, 2).

Y2 receptors are attractive targets for drug design (1). Y2 receptor regulation may be useful in the treatment of several pathophysiological conditions (1, 2) including memory loss (111), epileptic seizure (72), pain (64), depression, hypertension, locomotor problems, sleep disturbances, eating disorders, sexual/reproductive disorders, nasal congestion (97), and diarrhea (112). A rigorous investigation of Y2-related pathophysiology has been hindered by the absence of suitable non-peptide ligands. The chemical synthesis of subtype selective agonists and antagonists as potential drug candidates will be greatly accelerated by screening against a homogeneous population of cloned human Y2 receptors. As more specific pharmacological tools become available for probing receptor function, additional therapeutic indications are likely to be discovered.

We do not know whether the human and rat Y2 receptors we have discovered account for all of the pharmacological Y2 receptors so far described, or whether the Y2 receptor population is further divided into distinct receptor subtypes. Indeed, there is some suggestion of receptor heterogeneity within the Y2 receptor population (2). These are issues which can now be resolved using nucleotide sequence from the human Y2 receptor as the basis for in situ localization, anti-sense strategies, homology cloning, and related techniques. Such approaches will enable us to investigate the existence of potentially novel NPY receptor subtypes, in humans and other species, with additional pharmacologic and therapeutic significance.

TABLE 1: % aminoacid TM identity of the NPY-2 receptor with other 7 TM Receptors

m MUSGIR	42	h Y-1	41	
		h Y-4	41	
h 5HT1A	28	h Adenosine A2b	28	h
Substance K	33			
h 5HT2	31	h Adenosine A1	29	h
Substance P	32			
h α -adrenergic-1b	34	h Dopamine D1	31	h
Neurokinin-3	33			
h α -adrenergic-2a	34	h Dopamine D2	32	h
Interleukin-8 33				
h β -adrenergic-1	35	bov Hist H1	25	h
Angiotensin ₁	33	h Hist H2	28	h
Angiotensin ₂	27			m
Thyrotropin				
releasing hormone	27			h
Bradykinin	25			r
mas oncogene	20			

TABLE 2: Pharmacologically defined receptors for NPY and related pancreatic polypeptides.

Rank orders of affinity are based on published reports of binding and functional data (M9, M24, M3, M10). Missing peptides in the series reflect a lack of published information.

Receptor	Affinity (-pK _i or -pEC ₅₀)						
	11 to 10	10 to 9	9 to 8	8 to 7	7 to 6	< 6	
Y1	NPY PYY [Leu ³¹ , Pro ³⁴]NPY		NPY ₂₋₃₆	NPY ₁₃₋₃₆	PP		
Y2		PYY NPY NPY ₂₋₃₆	NPY ₁₃₋₃₆			[Leu ³¹ , Pro ³⁴]NPY PP	
Y3		NPY	[Pro ³⁴]NPY	NPY ₁₃₋₃₆ PP		PYY	
PP	PP		[Leu ³¹ , Pro ³⁴]NPY			NPY	

TABLE 3: Pharmacological profile of the CG-13 receptor.

Binding data reflect competitive displacement of ^{125}I -PYY from membranes of COS-7 cells transiently expressing CG-13 receptors. Peptides were tested at concentrations ranging from 0.001 nM to 100 nM. IC_{50} values corresponding to 50% displacement were determined by nonlinear regression analysis and converted to K_i values according to the equation, $K_i = \text{IC}_{50} / (1 + [\text{L}]/K_d)$, where $[\text{L}]$ is the ^{125}I -PYY concentration and K_d is the equilibrium dissociation constant of ^{125}I -PYY. The data shown are representative of at least two independent experiments.

15

Competitor	Human Y1, K_i (nM)	CG-13, K_i (nM)	SK-N-Be(2), K_i (nM)
human PYY	0.085 ± 0.021	0.39 ± 0.05	0.11 ± 0.02
human NPY	0.049 ± 0.009	0.69 ± 0.14	0.13 ± 0.02
porcine NPY ₂₋₃₆	1.4 ± 0.2	0.78 ± 0.13	0.41 ± 0.09
porcine NPY	0.049 ± 0.001	0.86 ± 0.13	0.28 ± 0.04
porcine PYY ₁₃₋₃₆	32 ± 7	1.5 ± 0.2	0.86 ± 0.14
porcine NPY ₁₈₋₃₆	28 ± 5	1.5 ± 0.2	2.1 ± 0.5
porcine NPY ₁₃₋₃₆	51 ± 16	2.4 ± 0.4	1.8 ± 0.4
porcine NPY ₂₀₋₃₆	62 ± 6	3.4 ± 0.3	3.1 ± 0.6
porcine NPY ₁₆₋₃₆	45 ± 4	3.8 ± 0.7	5.0 ± 0.5
porcine NPY ₂₂₋₃₆	170 ± 30	4.6 ± 0.1	3.2 ± 0.6

5

10

Table 3 continued			
Competitor	Human Y1, K ₁ (nM)	CG-13, K ₁	SK-N-Be(2) K ₁ (nM)
porcine NPY ₂₆₋₃₆	> 300	210 ± 60	70 ± 7
human NPY free acid	> 300	> 300	280 ± 120
human PP	200 ± 70	> 300	> 300
human [Leu ³¹ , Pro ³⁴] NPY	0.13 ± 0.02	> 300	> 300

TABLE 4: Extended pharmacological binding profile of the human Y2 receptor vs. other Y-type receptors cloned from human.

Binding data reflect competitive displacement of ^{125}I -PYY from membranes of COS-7 cells transiently expressing human Y1, human Y2, and human Y4 receptors. IC_{50} values corresponding to 50% displacement were determined by nonlinear regression analysis and converted to K_i values according to the equation Chang-Prusoff equation, $K_i = \text{IC}_{50}/(1 + [\text{L}]/K_d)$, where $[\text{L}]$ is the ^{125}I -PYY concentration and K_d is the equilibrium dissociation constant of ^{125}I -PYY. Any peptide not included in initial characterization shown in previous tables is referred to as a "new peptide". Data shown are representative of at least two independent experiments.

Peptide	Y1	Y2	Y4	Comments
NPY, human	0.08	0.74	2.2	
NPY, porcine	0.07	0.81	1.1	
NPY, frog (melanostatin)	0.07	0.87	1.2	new peptide
O-Me-Tyr ²¹ -NPY, human	0.12	1.6	6.1	new peptide
C2-NPY, porcine	73	3.5	120	new peptide
NPY ₂₋₃₆ , human	3.6	2.0	16	new peptide
NPY ₂₋₃₆ , porcine	2.4	1.2	5.6	
NPY ₁₃₋₃₆ , porcine	70	2.5	38	
NPY ₁₆₋₃₆ , porcine	41	3.6	54	
NPY ₁₈₋₃₆ , porcine	70	4.2	> 300	
NPY ₂₀₋₃₆ , porcine	63	3.6	120	
NPY ₂₂₋₃₆ , porcine	> 1000	18	> 990	
NPY ₂₆₋₃₆ , porcine	> 1000	380	300	

Table 4 continued					
	Peptide	Y1	Y2	Y4	Comments
5	[Leu ³¹ , Pro ³⁴]NPY, human	0.15	> 130	1.1	
	[Leu ³¹ , Pro ³⁴]NPY, porcine	0.15	> 540	1.5	new peptide
10	NPY free acid, human	490	> 1000	> 1000	
	NPY ₁₋₂₄ amide, human	> 1000	> 1000	> 1000	new peptide
15	[D- Trp ³²]NPY, human	> 1000	> 1000	> 1000	new peptide
	PYY, human	0.19	0.36	0.87	
	PYY, porcine	0.14	0.35	1.3	new peptide
20	PYY ₃₋₃₆ , human	45	0.70	14	new peptide
	PYY ₁₃₋₃₆ , porcine	33	1.5	46	
25	[Pro ³⁴]PYY, human	0.14	> 310	0.12	new peptide
	PP, human	77	> 1000	0.06	
	PP, bovine	240	> 830	0.05	new peptide
	PP, rat	460	> 1000	0.18	new peptide
30	PP, avian	400	> 1000	7.0	new peptide
	PP, frog	98	> 1000	61	new peptide
	PP, salmon	0.20	0.17	3.2	new peptide

Table 4 continued				
Peptide	Y1	Y2	Y3	Comments
[Ile ³¹ , Gln ³⁴] ^{PP} , human	> 86	20	0.09	new peptide
PYX-1	507	684	794	new peptide
PYX-2	> 1000	> 1000	> 1000	new peptide

TABLE 5: Macrolocalization of human Y2 receptor mRNA in human tissues by PCR.

Localization data reflect PCR-based amplification of human Y2 cDNA derived from mRNA extracts of human tissues. Southern blots of the PCR products were prepared and hybridized with ³²P-labeled oligonucleotide probes selective for Y-type receptor subtypes. The labeled products were recorded on X-ray film and the relative signal density was determined by visual inspection. In this rating scheme, + = faint signal, ++ = moderate signal, +++ = intense signal.

Human tissues	Human Y2 PCR Product
total brain	+++
frontal brain	++
ventricle (heart)	++
atrium (heart)	(-)
thoracic aorta	+++
coronary artery	++ ½
nasal mucosa	+
mesentery	++
stomach	++
ileum	++
pancreas	+
liver	(-)
kidney	+
bladder	+ ½
penis	+++
testes	not determined
uterus (endometrium)	(-)
uterus (myometrium)	(-)

TABLE 6: Peptide binding profile of the rat Y2a receptor vs. the human Y2 receptor.

Binding data reflect competitive displacement of ^{125}I -PYY from membranes of COS-7 cells transiently expressing rat Y2a and human Y2 receptors. IC_{50} values corresponding to 50% displacement were determined by nonlinear regression analysis and converted to K_i values according to the equation Chang-Prusoff equation, $K_i = \text{IC}_{50}/(1 + [\text{L}]/K_d)$, where $[\text{L}]$ is the ^{125}I -PYY concentration and K_d is the equilibrium dissociation constant of ^{125}I -PYY. Data shown are representative of at least two independent experiments.

Peptide	Rat Y2a	Human Y2
NPY, human	1.3	0.74
NPY ₂₋₃₆ , human	2.2	1.2
NPY ₁₃₋₃₆ , human	31	2.5
NPY ₂₀₋₃₆ , porcine	93	3.6
NPY ₂₆₋₃₆ , porcine	> 830	380
NPY free acid, human	> 980	> 1000
[Leu ³¹ , Pro ³⁴]NPY, human	> 1000	> 130
[D-Trp ³²]NPY, human	> 830	> 1000
PYY, porcine	0.28	0.35
PYY ₁₃₋₃₆ , porcine	1.5	28
PP, human	> 1000	> 1000
PP ₃₁₋₃₆ , human	> 10 000	> 10 000
PP, salmon	0.17	0.17
PP, bovine	> 1000	> 825
PP, rat	> 1000	> 1000

Table 7. Oligonucleotide probe sequences used for in situ hybridization

	<u>Probe</u>	<u>Sequence</u>	<u>Location</u>	<u>Orientation</u>	
5	KS972	5'-GGC CCA TTA GGT GCA GAG GCA GAT GAG AAT CAA ACT GTA GAA GTG- 3'	NH ₂ - terminus	sense	:
	KS974	5'-CAC TTC TAC AGT TTG ATT CTC ATC TGC CTC TGC ACC TAA TGG GCC- 3'	NH ₂ - terminus	antisense	:
	KS973	5'-CGG AGG TGT CCA TGA CCT TCA AGG CTA AAA AGA ACC TGG AAG TCA- 3'	COOH terminus	sense	
	KS975	5'-TGA CTT CCA GGT TCT TTT TAG CCT TGA AGG TCA TGG ACA CCT CCG- 3'	COOH terminus	antisense	

Table 8. Distribution of NPY Y2 mRNA in the rat CNS. Positive hybridization signals are indicated by "+" signs, no signal by "-", and a low signal by "+/-".

	Region	Hybridization	Region	Hybridization
5	Cortex			
	layer 2	-	Hypothalamus, cont.	
	layer 6	-	tuberal	+
	piriform	+		
10	entorhinal	-	Thalamus	
	cingulate	-	anterior nuclei	-
	Olfactory bulb	-	paraventricular n.	+
	Anterior olfactory n.	-	rhomboid n.	-
15	Basal ganglia		reuniens n.	-
	caudate-putamen	+/-	mediodorsal n.	-
	n. accumbens	-	ventral nuclei	-
	olfactory tubercle	+	reticular n.	-
20	globus pallidus	-	centrolateral n.	-
	islands of Calleja	-	centromedial n.	+
	Septal area		zona incerta	-
	lateral septum	+	lateral posterior n.	-
25	medial septum	-	lateral dorsal n.	-
	septohippocampal	-	posterior n.	-
	diagonal band n.	-	medial geniculate n.	-
	Clastrum	-	dorsal lateral gen.	-
30	Dorsal endopiriform	-	ventral lateral gen.	-
	Hypothalamus		habenula	-
	anterior	-	Hippocampus	
35	paraventricular	+	CA1	-
	dorsomedial	+	CA2	-
	ventromedial	+	CA3	+
	arcuate	+	subiculum	-
	lateral	-	presubiculum	-
40	mammillary	+	parasubiculum	-
			Dentate gyrus	
			granule cell layer	-
			polymorph layer	-
45				
50				

Table 8 (continued from previous page)

	Region	Hybridization	Region	Hybridization
			Pons/medulla cont.	
			dorsal vagus	NA
			hypoglossal	NA
5	Amygdala			
	anterior	-	Cerebellum	
	medial	+	granule cell layer	-
	cortical	+	molecular layer	-
10	amygdalohipp.	-	Purkinje cells	-
	basomedial	+	deep nuclei	-
	basolateral	-		
	lateral	-	Spinal cord	
	central	+	dorsal horn	-
15	bed nucleus	-	ventral horn	+
			intermediolateral	-
	Midbrain			
	superior colliculus	-	Dorsal root ganglia	+
	inferior colliculus	-		
20	mes. trigeminal	-		
	dorsal raphe	+		
	caudal linear raphe	+		
	median raphe	-		
	raphe magnu	-		
25	substantia nigra	-		
	central gray	-		
	Pons/medulla			
	locus coeruleus	-		
30	subcoeruleus	-		
	parabrachial n.	-		
	facial n.	-		
	pontine n.	+		
	pontine ret. n.	-		
35	reticulotegmental	+		
	A5	-		
	A7	-		
	gigantocellular	-		
	lateral reticular n.	-		
40	motor trigeminal	NA		
	spinal trigeminal	NA		
	medial vestibular	-		
	solitarius	NA		
45				

Abbreviations

	1-9	spinal cord laminae
	Arc	arcuate n. hypothalamus
	BMP	posterior basomedial n. amygdala
5	CA3	field CA3 of the hippocampus
	CC	central canal
	Cli	caudal linear raphe n.
	CM	centromedial n. thalamus
	DMH	dorsomedial n. hypothalamus
10	DR	dorsal raphe n.
	LSV	lateral septum, ventral
	Me	medial n. amygdala
	MeAV	medial n. amygdala, anteroventral division
	PDTg	posterior dorsal tegmental n.
15	Pir	piriform cortex
	PMD	dorsal preammillary n.
	PMCo	posterior medial cortical n. amygdala
	Pn	pontine n.
	PVH	paraventricular n. hypothalamus
20	PVT	paraventricular n. thalamus
	TC	tuber cinereum
	TuO	olfactory tubercle
	VMH	ventromedial n. hypothalamus
25		

TABLE 9: Functional activation of the human Y2 receptor and inhibition of cAMP accumulation.

K_i values were derived from binding assays as described in Table 1. Peptides were evaluated for binding affinity and then analyzed for functional activity. Functional data were derived from radioimmunoassay of cAMP accumulation in stably transfected 293 cells stimulated with 10 μ M forskolin. The maximum inhibition of cAMP accumulation relative to that produced by human NPY (E_{max}) and the concentration producing a half-maximal effect (EC_{50}) were determined by nonlinear regression. Data shown are representative of at least two independent experiments.

	Peptide	Binding	Function	
		K_i (nM)	EC_{50} (nM)	E_{max}
	NPY, human	0.74	0.25	100 %
	NPY, porcine	0.81	0.20	113%
	C2-NPY, porcine	3.5	0.14	116 %
20	NPY ₂₋₃₆ , human	2.0	0.35	94%
	NPY ₂₋₃₆ , porcine	1.2	1.2	96%
	NPY ₁₃₋₃₆ , porcine	2.5	1.7	110 %
25	NPY ₁₆₋₃₆ , porcine	3.6	1.8	92 %
	NPY ₁₈₋₃₆ , porcine	4.2	2.1	92 %
30	NPY ₂₀₋₃₆ , porcine	3.6	3.2	77 %
	NPY ₂₂₋₃₆ , porcine	18	2.3	88 %
35	[Leu ³¹ , Pro ³⁶]NPY, human	> 130	> 3000	not determined
	[Leu ³¹ , Pro ³⁶]NPY, porcine	> 540	> 3000	not determined
40	[D-Trp ³²]NPY, human	> 1000	> 3000	not determined
	PYY, human	0.36	0.31	100 %

Table 9 continued			
Peptide	Binding	Function	
	K ₁ (nM)	EC ₅₀ (nM)	E _{max}
PYY, porcine	0.35	0.16	103 %
PYY ₃₋₃₆ , human	0.70	0.22	99 %
PYY ₁₃₋₃₆ , porcine	1.5	0.13	102 %
[Pro ³⁴]PYY, human	> 310	> 120	not determined
PP, salmon	0.17	0.07	79 %
PYX-1	684	> 3000	not determined
PYX-2	> 1000	> 3000	not determined

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Synaptic Pharmaceutical Corporation

(ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP

(B) STREET: 1185 Avenue of the Americas

(C) CITY: New York

(D) STATE: New York

(E) COUNTRY: U.S.A.

(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.

(B) REGISTRATION NUMBER: 28,678

(C) REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-278-0400

(B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1280 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 43..1185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTCTTGTG CTGGTTGCAG GCCAAGTGGA CCTGTACTGA AA ATG GGT CCA ATA
54 Met Gly Pro Ile
1

GGT GCA GAG GCT GAT GAG AAC CAG ACA GTG GAA GAA ATG AAG GTG GAA
102
Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Glu Met Lys Val Glu

114

	5	10	15	20
	CAA TAC GGG CCA CAA ACA ACT CCT AGA GGT GAA CTG GTC CCT GAC CCT			
5	150 Gln Tyr Gly Pro Gln Thr Thr Pro Arg Gly Glu Leu Val Pro Asp Pro	25	30	35
	GAG CCA GAG CTT ATA GAT AGT ACC AAG CTG ATT GAG GTA CAA GTT GTT			
10	198 Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Ile Glu Val Gln Val Val	40	45	50
	CTC ATA TTG GCC TAC TGC TCC ATC ATC TTG CTT GGG GTA ATT GGC AAC			
15	246 Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly Val Ile Gly Asn	55	60	65
	TCC TTG GTG ATC CAT GTG GTG ATC AAA TTC AAG AGC ATG CGC ACA GTA			
20	294 Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser Met Arg Thr Val	70	75	80
	ACC AAC TTT TTC ATT GCC AAT CTG GCT GTG GCA GAT CTT TTG GTG AAC			
25	342 Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp Leu Leu Val Asn	85	90	95
	ACT CTG TGT CTA CCG TTC ACT CTT ACC TAT ACC TTA ATG GGG GAG TGG			
30	390 Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu Met Gly Glu Trp	105	110	115
	AAA ATG GGT CCT GTC CTG TGC CAC CTG GTG CCC TAT GCC CAG GGC CTG			
35	438 Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr Ala Gln Gly Leu	120	125	130
	GCA GTA CAA GTA TCC ACA ATC ACC TTG ACA GTA ATT GCC CTG GAC CGG			
40	486 Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile Ala Leu Asp Arg	135	140	145
	CAC AGG TGC ATC GTC TAC CAC CTA GAG AGC AAG ATC TCC AAG CGA ATC			
45	534 His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile Ser Lys Arg Ile	150	155	160
	AGC TTC CTG ATT ATT GGC TTG GCC TGG GGC ATC AGT GCC CTG CTG GCA			
50	582 Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Ile Ser Ala Leu Leu Ala	165	170	175
	AGT CCC CTG GCC ATC TTC CGG GAG TAT TCG CTG ATT GAG ATC ATC CCG			
55	630 Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile Glu Ile Ile Pro	185	190	195
	GAC TTT GAG ATT GTG GCC TGT ACT GAA AAG TGG CCT GGC GAG GAG AAG			
60	678 Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro Gly Glu Glu Lys	200	205	210
	AGC ATC TAT GGC ACT GTC TAT AGT CTT TCT TCC TTG TTG ATC TTG TAT			
65	726 Ser Ile Tyr Gly Thr Val Tyr Ser Leu Ser Ser Leu Leu Ile Leu Tyr	215	220	225

115

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5      GTT TTG CCT CTG GGC ATT ATA TCA TTT TCC TAC ACT CGC ATT TGG AGT
      774
      Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr Arg Ile Trp Ser
      230                235                240

10     AAA TTG AAG AAC CAT GTC AGT CCT GGA GCT GCA AAT GAC CAC TAC CAT
      822
      Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Asn Asp His Tyr His
      245                250                255                260

15     CAG CGA AGG CAA AAA ACC ACC AAA ATG CTG GTG TGT GTG GTG GTG GTG
      870
      Gln Arg Arg Gln Lys Thr Thr Lys Met Leu Val Cys Val Val Val Val
      265                270                275

20     TTT GCG GTC AGC TGG CTG CCT CTC CAT GCC TTC CAG CTT GCC GTT GAC
      918
      Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln Leu Ala Val Asp
      280                285                290

25     ATT GAC AGC CAG GTC CTG GAC CTG AAG GAG TAC AAA CTC ATC TTC ACA
      966
      Ile Asp Ser Gln Val Leu Asp Leu Lys Glu Tyr Lys Leu Ile Phe Thr
      295                300                305

30     GTG TTC CAC ATC ATC GCC ATG TGC TCC ACT TTT GCC AAT CCC CTT CTC
      1014
      Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala Asn Pro Leu Leu
      310                315                320

35     TAT GGC TGG ATG AAC AGC AAC TAC AGA AAG GCT TTC CTC TCG GCC TTC
      1062
      Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe Leu Ser Ala Phe
      325                330                335                340

40     CGC TGT GAG CAG CGG TTG GAT GCC ATT CAC TCT GAG GTG TCC GTG ACA
      1110
      Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu Val Ser Val Thr
      345                350                355

45     TTC AAG GCT AAA AAG AAC CTG GAG GTC AGA AAG AAC AGT GGC CCC AAT
      1158
      Phe Lys Ala Lys Lys Asn Leu Glu Val Arg Lys Asn Ser Gly Pro Asn
      360                365                370

50     GAC TCT TTC ACA GAG GCT ACC AAT GTC TAAGGAAGCT GTGGTGTGAA
      1205
      Asp Ser Phe Thr Glu Ala Thr Asn Val
      375                380

55     AATGTATGGA TGAATTCTGA CCAGAGCTAT GAATCTGGTT GATGGCGGCT CACAAGTGAA
      1265

      AACTGATTTC CCATT
      1280

```

(2) INFORMATION FOR SEQ ID NO:2:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 65 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

116

	Met	Gly	Pro	Ile	Gly	Ala	Glu	Ala	Asp	Glu	Asn	Gln	Thr	Val	Glu	Glu	
	1				5					10					15		
5	Met	Lys	Val	Glu	Gln	Tyr	Gly	Pro	Gln	Thr	Thr	Pro	Arg	Gly	Glu	Leu	
				20					25					30			
	Val	Pro	Asp	Pro	Glu	Pro	Glu	Leu	Ile	Asp	Ser	Thr	Lys	Leu	Ile	Glu	
			35					40					45				
10	Val	Gln	Val	Val	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile	Ile	Leu	Leu	Gly	
		50					55					60					
	Val	Ile	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile	Lys	Phe	Lys	Ser	
15		65				70					75					80	
	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu	Ala	Val	Ala	Asp	
					85					90					95		
20	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu	Thr	Tyr	Thr	Leu	
				100					105					110			
	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His	Leu	Val	Pro	Tyr	
			115					120					125				
25	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr	Leu	Thr	Val	Ile	
		130					135					140					
	Ala	Leu	Asp	Arg	His	Arg	Cys	Ile	Val	Tyr	His	Leu	Glu	Ser	Lys	Ile	
30		145				150					155					160	
	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala	Trp	Gly	Ile	Ser	
					165					170					175		
35	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu	Tyr	Ser	Leu	Ile	
				180					185					190			
	Glu	Ile	Ile	Pro	Asp	Phe	Glu	Ile	Val	Ala	Cys	Thr	Glu	Lys	Trp	Pro	
			195					200					205				
40	Gly	Glu	Glu	Lys	Ser	Ile	Tyr	Gly	Thr	Val	Tyr	Ser	Leu	Ser	Ser	Leu	
		210					215					220					
	Leu	Ile	Leu	Tyr	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ser	Phe	Ser	Tyr	Thr	
45		225				230					235					240	
	Arg	Ile	Trp	Ser	Lys	Leu	Lys	Asn	His	Val	Ser	Pro	Gly	Ala	Ala	Asn	
					245					250					255		
50	Asp	His	Tyr	His	Gln	Arg	Arg	Gln	Lys	Thr	Thr	Lys	Met	Leu	Val	Cys	
				260					265					270			
	Val	Val	Val	Val	Phe	Ala	Val	Ser	Trp	Leu	Pro	Leu	His	Ala	Phe	Gln	
			275					280					285				
55	Leu	Ala	Val	Asp	Ile	Asp	Ser	Gln	Val	Leu	Asp	Leu	Lys	Glu	Tyr	Lys	
		290					295					300					
	Leu	Ile	Phe	Thr	Val	Phe	His	Ile	Ile	Ala	Met	Cys	Ser	Thr	Phe	Ala	
60		305				310					315					320	
	Asn	Pro	Leu	Leu	Tyr	Gly	Trp	Met	Asn	Ser	Asn	Tyr	Arg	Lys	Ala	Phe	
					325					330					335		
65	Leu	Ser	Ala	Phe	Arg	Cys	Glu	Gln	Arg	Leu	Asp	Ala	Ile	His	Ser	Glu	
			340					345						350			
	Val	Ser	Val	Thr	Phe	Lys	Ala	Lys	Lys	Asn	Leu	Glu	Val	Arg	Lys	Asn	

117

355

360

365

Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn Val
 370 375 380

5

(2) INFORMATION FOR SEQ ID NO:3:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 211..1353

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGTGTTAACA GACTCGTGTA AAGGATTGTC TTTATGGAGC TTTTATGAGA TCTGTGGTGT
 60

30

GATGAATCAG AACACAGCTA CGCAGAGGAG CTCAGCCTAA ACTAAATCAA CCCCTTTAGG
 120

35

ATGGTTCTCT GTTTCACTAA CTTTTTTTAA TGTCGTTTTC TGTATAGAT TCTTGTGCTA
 180

TCTGCAGGCC AAATTGGAAC TGAGGTGAAG ATG GGC CCA TTA GGT GCA GAG GCA
 234

40

Met Gly Pro Leu Gly Ala Glu Ala
 1 5

GAT GAG AAT CAA ACT GTA GAA GTG AAA GTG GAA CTC TAT GGG TCG GGG
 282

45

Asp Glu Asn Gln Thr Val Glu Val Lys Val Glu Leu Tyr Gly Ser Gly
 10 15 20

CCC ACC ACT CCT AGA GGT GAG TTG CCC CCT GAT CCA GAG CCG GAG CTC
 330

50

Pro Thr Thr Pro Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu
 25 30 35 40

ATA GAC AGC ACC AAA CTG GTT GAG GTG CAG GTG GTC CTT ATA CTG GCC
 378

55

Ile Asp Ser Thr Lys Leu Val Glu Val Gln Val Val Leu Ile Leu Ala
 45 50 55

TAT TGT TCC ATC ATC TTG CTG GGC GTA GTT GGC AAC TCT CTG GTA ATC
 426

60

Tyr Cys Ser Ile Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile
 60 65 70

CAT GTG GTG ATC AAA TTC AAG AGC ATG CGC ACA GTA ACC AAC TTT TTT
 474

65

His Val Val Ile Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe
 75 80 85

ATT GCC AAC CTG GCT GTG GCG GAT CTT TTG GTG AAC ACC CTG TGC CTG

118

522
 Ile Ala Asn Leu Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu
 90 95 100

5 CCA TTC ACT CTT ACC TAT ACC TTG ATG GGG GAG TGG AAA ATG GGT CCA
 570
 Pro Phe Thr Leu Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro
 105 110 115 120

10 GTT TTG TGC CAT TTG GTG CCC TAT GCC CAG GGT CTG GCA GTA CAA GTG
 618
 Val Leu Cys His Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val
 125 130 135

15 TCC ACA ATA ACT TTG ACA GTC ATT GCT TTG GAC CGA CAT CGT TGC ATT
 666
 Ser Thr Ile Thr Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile
 140 145 150

20 GTC TAC CAC CTG GAG AGC AAG ATC TCC AAG CAA ATC AGC TTC CTG ATT
 714
 Val Tyr His Leu Glu Ser Lys Ile Ser Lys Gln Ile Ser Phe Leu Ile
 155 160 165

25 ATT GGC CTG GCG TGG GGT GTC AGC GCT CTG CTG GCA AGT CCC CTT GCC
 762
 Ile Gly Leu Ala Trp Gly Val Ser Ala Leu Leu Ala Ser Pro Leu Ala
 170 175 180

30 ATC TTC CGG GAG TAC TCA CTG ATT GAG ATT ATT CCT GAC TTT GAG ATT
 810
 Ile Phe Arg Glu Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile
 185 190 195 200

35 GTA GCC TGT ACT GAG AAA TGG CCC GGG GAG GAG AAG AGT GTG TAC GGT
 858
 Val Ala Cys Thr Glu Lys Trp Pro Gly Glu Glu Lys Ser Val Tyr Gly
 205 210 215

40 ACA GTC TAC AGC CTT TCC ACC CTG CTA ATC CTC TAC GTT TTG CCT CTG
 906
 Thr Val Tyr Ser Leu Ser Thr Leu Leu Ile Leu Tyr Val Leu Pro Leu
 220 225 230

45 GGC ATC ATA TCT TTC TCC TAC ACC CGG ATC TGG AGT AAG CTA AAG AAC
 954
 Gly Ile Ile Ser Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn
 235 240 245

50 CAC GTT AGT CCT GGA GCT GCA AGT GAC CAT TAC CAT CAG CGA AGG CAC
 1002
 His Val Ser Pro Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His
 250 255 260

55 AAA ACG ACC AAA ATG CTC GTG TGC GTG GTA GTG GTG TTT GCA GTC AGC
 1050
 Lys Thr Thr Lys Met Leu Val Cys Val Val Val Val Phe Ala Val Ser
 265 270 275 280

60 TGG CTG CCC CTC CAT GCC TTC CAA CTT GCT GTG GAC ATC GAC AGC CAT
 1098
 Trp Leu Pro Leu His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His
 285 290 295

65 GTC CTG GAC CTG AAG GAG TAC AAA CTC ATC TTC ACC GTG TTC CAC ATT
 1146
 Val Leu Asp Leu Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile

119

300

305

310

ATT GCG ATG TGC TCC ACC TTC GCC AAC CCC CTT CTC TAT GGC TGG ATG
 1194
 5 Ile Ala Met Cys Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met
 315 320 325
 AAC AGC AAC TAC AGA AAA GCT TTC CTC TCA GCC TTC CGC TGT GAG CAG
 1242
 10 Asn Ser Asn Tyr Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln
 330 335 340
 AGG TTG GAT GCC ATT CAC TCG GAG GTG TCC ATG ACC TTC AAG GCT AAA
 1290
 15 Arg Leu Asp Ala Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys
 345 350 355 360
 AAG AAC CTG GAA GTC AAA AAG AAC AAT GGC CTC ACT GAC TCT TTT TCA
 1338
 20 Lys Asn Leu Glu Val Lys Lys Asn Asn Gly Leu Thr Asp Ser Phe Ser
 365 370 375
 GAG GCC ACC AAC GTG TAAGAATGCT GTGAAAGTAC GTGGGTAAAT TGCGACCAGA
 1393
 25 Glu Ala Thr Asn Val
 380
 GTTGCCAACC TGTTTAGGGA AGGTTTTCTG GCTAGTGCAT GCCACCTCCC ATTGTATTGA
 1453
 30 CCCTAAAAGC ATCAGAGTGG AAGCCCCAGC GGTATTGTTC CTGGAAAACCT GGCTGGAAGA
 1513
 ATGAGGAGAA AATAAACAGA TTGCTGTGGC GCAACGTTCT GAT
 1556
 35

(2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 50 Met Gly Pro Leu Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Val
 1 5 10 15
 Lys Val Glu Leu Tyr Gly Ser Gly Pro Thr Thr Pro Arg Gly Glu Leu
 20 25 30
 55 Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Val Glu
 35 40 45
 Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly
 50 55 60
 60 Val Val Gly Asn Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser
 65 70 75 80
 65 Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp
 85 90 95
 Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu

120

	100	105	110
	Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr		
5	115	120	125
	Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile		
	130	135	140
10	Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile		
	145	150	155
	Ser Lys Gln Ile Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Val Ser		
	165	170	175
15	Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile		
	180	185	190
	Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro		
20	195	200	205
	Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser Leu Ser Thr Leu		
	210	215	220
25	Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr		
	225	230	235
	Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Ser		
	245	250	255
30	Asp His Tyr His Gln Arg Arg His Lys Thr Thr Lys Met Leu Val Cys		
	260	265	270
	Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln		
35	275	280	285
	Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu Lys Glu Tyr Lys		
	290	295	300
40	Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala		
	305	310	315
	Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe		
	325	330	335
45	Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu		
	340	345	350
	Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu Val Lys Lys Asn		
50	355	360	365
	Asn Gly Leu Thr Asp Ser Phe Ser Glu Ala Thr Asn Val		
	370	375	380

(2) INFORMATION FOR SEQ ID NO:5:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: genomic DNA
- (iii) HYPOTHETICAL: NO
- 65 (iv) ANTI-SENSE: NO

121

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 55..1200

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

10  TTTCTGTTAT AGATTCTTGT GCTATCTGCA GGCCAAATTG GAACTGAGGT GAAG ATG
    57
                                     Met
                                     1
15  GGC CCA TTA GGT GCA GAG GCA GAT GAG AAT CAA ACT GTA GAA GTG AAA
    105
    Gly Pro Leu Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Val Lys
        5              10              15
20  GTG GAA TTC TAT GGG TCG GGG CCC ACC ACT CCT AGA GGT GAG TTG CCC
    153
    Val Glu Phe Tyr Gly Ser Gly Pro Thr Thr Pro Arg Gly Glu Leu Pro
        20              25              30
25  CCT GAT CCA GAG CCG GAG CTC ATA GAC AGC ACC AAA CTG GTT GAG GTG
    201
    Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Val Glu Val
        35              40              45
30  CAG GTG GTC CTT ATA CTG GCC TAT TGT TCC ATC ATC TTG CTG GGC GTA
    249
    Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly Val
        50              55              60              65
35  GTT GGC AAC TCT CTG GTA ATC CAT GTG GTG ATC AAA TTC AAG AGC ATG
    297
    Val Gly Asn Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser Met
        70              75              80
40  CGC ACA GTA ACC AAC TTT TTT ATT GCC AAC CTG GCT GTG GCG GAT CTT
    345
    Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp Leu
        85              90              95
45  TTG GTG AAC ACC CTG TGC CTG CCA TTC ACT CTT ACC TAT ACC TTG ATG
    393
    Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu Met
        100              105              110
50  GGG GAG TGG AAA ATG GGT CCA GTT TTG TGC CAT TTG GTG CCC TAT GCC
    441
    Gly Glu Trp Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr Ala
        115              120              125
55  CAG GGT CTG GCA GTA CAA GTG TCC ACA ATA ACT TTG ACA GTC ATT GCT
    489
    Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile Ala
        130              135              140              145
60  TTG GAC CGA CAT CGT TGC ATT GTC TAC CAC CTG GAG AGC AAG ATC TCC
    537
    Leu Asp Arg His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile Ser
        150              155              160
65  AAG CAA ATC AGC TTC CTG ATT ATT GGC CTG GCG TGG GGT GTC AGC GCT
    585
    Lys Gln Ile Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Val Ser Ala
        165              170              175

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122

CTG CTG GCA AGT CCC CTT GCC ATC TTC CGG GAG TAC TCA CTG ATT GAG
 633
 Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile Glu
 180 185 190
 5
 ATT ATT CCT GAC TTT GAG ATT GTA GCC TGT ACT GAG AAA TGG CCC GGG
 681
 Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro Gly
 195 200 205
 10
 GAG GAG AAG AGT GTG TAC GGT ACA GTC TAC AGC CTT TCC ACC CTG CTA
 729
 Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser Leu Ser Thr Leu Leu
 210 215 220 225
 15
 ATC CTC TAC GTT TTG CCT CTG GGC ATC ATA TCT TTC TCC TAC ACC CGG
 777
 Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr Arg
 230 235 240
 20
 ATC TGG AGT AAG CTA AAG AAC CAC GTT AGT CCT GGA GCT GCA AGT GAC
 825
 Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Ser Asp
 245 250 255
 25
 CAT TAC CAT CAG CGA AGG CAC AAA ATG ACC AAA ATG CTC GTG TGC GTG
 873
 His Tyr His Gln Arg Arg His Lys Met Thr Lys Met Leu Val Cys Val
 260 265 270
 30
 GTA GTG GTG TTT GCA GTC AGC TGG CTG CCC CTC CAT GCC TTC CAA CTT
 921
 Val Val Val Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln Leu
 275 280 285
 35
 GCT GTG GAC ATC GAC AGC CAT GTC CTG GAC CTG AAG GAG TAC AAA CTC
 969
 Ala Val Asp Ile Asp Ser His Val Leu Asp Leu Lys Glu Tyr Lys Leu
 290 295 300 305
 40
 ATC TTC ACC GTG TTC CAC ATT ATT GCG ATG TGC TCC ACC TTC GCC AAC
 1017
 Ile Phe Thr Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala Asn
 310 315 320
 45
 CCC CTT CTC TAT GGC TGG ATG AAC AGC AAC TAC AGA AAA GCT TTC CTC
 1065
 Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe Leu
 325 330 335
 50
 TCA GCC TTC CGC TGT GAG CAG AGG TTG GAT GCC ATT CAC TCG GAG GTG
 1113
 Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu Val
 340 345 350
 55
 TCC ATG ACC TTC AAG GCT AAA AAG AAC CTG GAA GTC AAA AAG AAC AAT
 1161
 Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu Val Lys Lys Asn Asn
 355 360 365
 60
 GGC CTC ACT GAC TCT TTT TCA GAG GCC ACC AAC GTG TAA
 1200
 Gly Leu Thr Asp Ser Phe Ser Glu Ala Thr Asn Val *
 370 375 380
 65

(2) INFORMATION FOR SEQ ID NO:6:

123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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10  Met Gly Pro Leu Gly Ala Glu Ala Asp Glu Asn Gln Thr Val Glu Val
      1      5      10      15
    Lys Val Glu Phe Tyr Gly Ser Gly Pro Thr Thr Pro Arg Gly Glu Leu
      20      25      30
15  Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr Lys Leu Val Glu
      35      40      45
    Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile Ile Leu Leu Gly
      50      55      60
20  Val Val Gly Asn Ser Leu Val Ile His Val Val Ile Lys Phe Lys Ser
      65      70      75      80
25  Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu Ala Val Ala Asp
      85      90      95
    Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu Thr Tyr Thr Leu
      100      105      110
30  Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His Leu Val Pro Tyr
      115      120      125
    Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr Leu Thr Val Ile
      130      135      140
35  Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu Glu Ser Lys Ile
      145      150      155      160
40  Ser Lys Gln Ile Ser Phe Leu Ile Ile Gly Leu Ala Trp Gly Val Ser
      165      170      175
    Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu Tyr Ser Leu Ile
      180      185      190
45  Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr Glu Lys Trp Pro
      195      200      205
50  Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser Leu Ser Thr Leu
      210      215      220
    Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser Phe Ser Tyr Thr
      225      230      235      240
55  Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro Gly Ala Ala Ser
      245      250      255
    Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys Met Leu Val Cys
      260      265      270
60  Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu His Ala Phe Gln
      275      280      285
    Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu Lys Glu Tyr Lys
      290      295      300
65  Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys Ser Thr Phe Ala

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305 310 315 320

Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe
325 330 335

5 Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala Ile His Ser Glu
340 345 350

10 Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu Val Lys Lys Asn
355 360 365

Asn Gly Leu Thr Asp Ser Phe Ser Glu Ala Thr Asn Val *

370 375 380

15 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAAGTTGTTC TCATATTGGC CTACTGCTCC ATCATCTTGC TTGGGGTAAT
50

35 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCACCACAT GGATCACCAA GGAGTTGCCA ATTACCCCAA GCAAGATGAT
50

55 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: DNA (genomic)

65 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5 TTTTTCATTG CCAATCTGGC TGTGGCAGAT CTTTGGTGA ACACT
45

(2) INFORMATION FOR SEQ ID NO:10:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 AGGTAAGAGT GAACGGTAGA CACAGAGTGT TCACCAAAG ATCTG
45

(2) INFORMATION FOR SEQ ID NO:11:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- 40 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

45 CCACCTGGTG CCCTATGCCC AGGGCCTGGC AGTACAAGTA TCCAC
50 45

(2) INFORMATION FOR SEQ ID NO:12:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 65

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGGGCAATT ACTGTCAAGG TGATTGTGGA TACTTGACT GCCAG
45

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

15

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATCAGCTTC CTGATTATTG GCTTGGCCTG GGGCATCAGT GCCCT
45

25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

35

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGATGGCC AGGGGACTTG CCAGCAGGGC ACTGATGCCC CAGGC
45

50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)

60

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

127

ACTGTCTATA GTCTTTCTTC CTTGTTGATC TTGTATGTTT TGCCT
45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTAGGAAAA TGATATAATG CCCAGAGGCA AAACATACAA GATCA
45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGGTGTGTG TGGTGGTGGT GTTGCGGTC AGCTGGCTGC CTCTC
45

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTCAACGGC AAGCTGGAAG GCATGGAGAG GCAGCCAGCT GACCG

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45

(2) INFORMATION FOR SEQ ID NO:19:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCATCTTCA CAGTGTTCCA CATCATCGCC ATGTGCTCCA CTTTTC
47

25 (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 35 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

45 TTCATCCAGC CATAGAGAAG GGGATTGGCA AAAGTGGAGC ACATGGC
47

50 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 60 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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GGGAGTATTC GCTGATTGAG ATCAT
25

(2) INFORMATION FOR SEQ ID NO:22:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 15 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCTTGAATG TCACGGACAC CTC
23

25 (2) INFORMATION FOR SEQ ID NO:23:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 35 (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

45 CTGATGGTAG TGGTCATTG CAGCTCCAGG ACTGACATGG TTCTT
45

What is claimed is:

- 5 1. An isolated nucleic acid molecule encoding a Y2 receptor.
2. An isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule is a DNA molecule.
- 10 3. An isolated DNA molecule of claim 2, wherein the DNA molecule is a cDNA molecule.
4. An isolated DNA molecule of claim 2, wherein the DNA molecule is a genomic DNA molecule.
- 15 5. An isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule is a RNA molecule.
- 20 6. An isolated nucleic acid molecule of claim 1 wherein the nucleic acid molecule encodes a human Y2 receptor.
- 25 7. An isolated nucleic acid molecule of claim 6 wherein the nucleic acid molecule encodes a receptor being characterized by an amino acid sequence in the transmembrane region, which amino acid sequence has 60% homology or higher to the amino acid sequence in the transmembrane region of the human Y2 receptor shown in Figure 11.
- 30 8. An isolated nucleic acid molecule of claim 6 wherein the human Y2 receptor has substantially the same amino acid sequence as shown in Figure 2.
- 35 9. An isolated nucleic acid molecule of claim 6 wherein

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the human Y2 receptor has the amino acid sequence as shown in Figure 2.

- 5 10. An isolated nucleic acid molecule of claim 1 wherein the nucleic acid molecule encodes a rat Y2 receptor.
11. An isolated nucleic acid molecule of claim 10 wherein the rat Y2 receptor has substantially the same amino acid sequence as shown in Figure 8.
- 10 12. An isolated nucleic acid molecule of claim 10 wherein the rat Y2 receptor has the amino acid sequence shown in Figure 8.
- 15 13. An isolated nucleic acid molecule of claim 10 wherein the rat Y2 receptor has substantially the same amino acid sequence as shown in Figure 9.
- 20 14. An isolated nucleic acid molecule of claim 10 wherein the rat Y2 receptor has the amino acid sequence shown in Figure 9.
15. An isolated, purified Y2 receptor protein.
- 25 16. A vector comprising the nucleic acid molecule of claim 1.
17. A vector comprising the nucleic acid molecule of claim 6.
- 30 18. A vector comprising the nucleic acid molecule of claim 10.
- 35 19. A vector of claim 16 adapted for expression in a bacterial cell which comprises the regulatory elements necessary for expression of the nucleic acid in the bacterial cell operatively linked to the

nucleic acid encoding the Y2 receptor as to permit expression thereof.

- 5 20. A vector of claim 16 adapted for expression in a yeast cell which comprises the regulatory elements necessary for expression of the nucleic acid in the yeast cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
- 10 21. A vector of claim 16 adapted for expression in an insect cell which comprises the regulatory elements necessary for expression of the nucleic acid in the insect cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
- 15 22. A vector of claim 21 wherein the vector is a baculovirus.
- 20 23. A vector of claim 16 adapted for expression in a mammalian cell which comprises the regulatory elements necessary for expression of the nucleic acid in the mammalian cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
- 25 24. A vector of claim 17 adapted for expression in a mammalian cell which comprises the regulatory elements necessary for expression of the nucleic acid in the mammalian cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
- 30 25. A vector of claim 24 wherein the vector is a plasmid.
- 35

26. The plasmid of claim 25 designated pcEXV-hY2 (ATCC Accession No. 75659).
27. A vector of claim 18 adapted for expression in a mammalian cell which comprises the regulatory elements necessary for expression of the nucleic acid in the mammalian cell operatively linked to the nucleic acid encoding the Y2 receptor as to permit expression thereof.
28. A vector of claim 27 wherein the vector is a plasmid.
29. The plasmid of claim 28 designated pcEXV-rY2a (ATCC Accession No. 97035).
30. The plasmid of claim 28 designated pcEXV-rY2b (ATCC Accession No. 97036).
31. A cell comprising the vector of either of claims 24 or 28.
32. The cell of claim 31 wherein the cell is a mammalian cell.
33. The cell of claim 32 wherein the mammalian cell is non-neuronal in origin.
34. The cell of claim 33 wherein the mammalian cell non-neuronal in origin is a COS-7 cell.
35. The cell of claim 33 wherein the mammalian cell non-neuronal in origin is a NIH-3T3 cell.
36. A NIH-3T3 cell of claim 36 designated N-hY2-5 (ATCC Accession No. CRL-11825).

37. The cell of claim 33 wherein the mammalian cell non-neuronal in origin is a 293 human embryonic kidney cell.
- 5 38. A 293 human embryonic kidney cell of claim 37 designated 293-hY2-10 (ATCC Accession No. 11837).
- 10 39. A nucleic acid probe comprising a nucleic acid molecule of at least 15 nucleotides capable of specifically hybridizing with a unique sequence included within the sequence of a nucleic acid molecule encoding a Y2 receptor.
- 15 40. The nucleic acid probe of claim 39 wherein the nucleic acid is DNA.
41. The nucleic acid probe of claim 39 wherein the nucleic acid encodes a human Y2 receptor.
- 20 42. The nucleic acid probe of claim 39 wherein the nucleic acid encodes a rat Y2 receptor.
- 25 43. An antisense oligonucleotide having a sequence capable of specifically hybridizing to an mRNA molecule encoding a Y2 receptor so as to prevent translation of the mRNA molecule.
- 30 44. An antisense oligonucleotide having a sequence capable of specifically hybridizing to the cDNA molecule of claim 3.
45. An antisense oligonucleotide of either of claims 43 or 44 comprising chemical analogues of nucleotides.
- 35 46. An antibody directed to a Y2 receptor.
47. An antibody of claim 46, wherein the Y2 receptor is

a human Y2 receptor.

48. An antibody of claim 46 wherein the Y2 receptor is a rat Y2 receptor.

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49. An antibody of claim 46, wherein the antibody is a monoclonal antibody.

10

50. A monoclonal antibody of claim 49 directed to an epitope of a Y2 receptor present on the surface of a Y2 receptor expressing cell.

15

51. A pharmaceutical composition comprising an amount of the oligonucleotide of claim 43 effective to decrease activity of a Y2 receptor by passing through a cell membrane and binding specifically with mRNA encoding a Y2 receptor in the cell so as to prevent its translation and a pharmaceutically acceptable carrier capable of passing through a cell membrane.

20

52. A pharmaceutical composition of claim 51, wherein the oligonucleotide is coupled to a substance which inactivates mRNA.

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53. A pharmaceutical composition of claim 52, wherein the substance which inactivates mRNA is a ribozyme.

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54. A pharmaceutical composition of claim 51, wherein the pharmaceutically acceptable carrier comprises a structure which binds to a receptor on a cell capable of being taken up by cells after binding to the structure.

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55. A pharmaceutical composition of claim 54, wherein the structure of the pharmaceutically acceptable carrier is capable of binding to a receptor which is

specific for a selected cell type.

56. A pharmaceutical composition comprising an amount of
the antibody of claim 46 effective to block binding
of a ligand to a Y2 receptor and a pharmaceutically
acceptable carrier.
57. A transgenic nonhuman mammal expressing nucleic acid
encoding a Y2 receptor.
58. A transgenic nonhuman mammal comprising a homologous
recombination knockout of the native Y2 receptor.
59. A transgenic nonhuman mammal whose genome comprises
antisense nucleic acid complementary to nucleic acid
encoding a Y2 receptor so placed as to be
transcribed into antisense mRNA which is
complementary to mRNA encoding a Y2 receptor and
which hybridizes to mRNA encoding a Y2 receptor
thereby reducing its translation.
60. The transgenic nonhuman mammal of either of claims
57 or 59, wherein the nucleic acid encoding a Y2
receptor additionally comprises an inducible
promoter.
61. The transgenic nonhuman mammal of either of claims
57 or 59, wherein the nucleic acid encoding a Y2
receptor additionally comprises tissue specific
regulatory elements.
62. A transgenic nonhuman mammal of any of claims 57, 58
or 59, wherein the transgenic nonhuman mammal is a
mouse.
63. A method for determining whether a ligand can bind
specifically to a Y2 receptor which comprises

contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting binding of ligands to such receptor, and detecting the presence of any such ligand bound specifically to the Y2 receptor, thereby determining whether the ligand binds specifically to a Y2 receptor.

64. A method of claim 63 wherein the Y2 receptor is a human Y2 receptor.
65. A method of claim 63 wherein the Y2 receptor is a rat Y2 receptor.
66. A method for determining whether a ligand can bind specifically to a Y2 receptor, which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting binding of ligands to such receptor, and detecting the presence of any such ligand specifically bound to the Y2 receptor, thereby determining whether the ligand binds specifically to a Y2 receptor, wherein the Y2 receptor is characterized by an amino acid sequence in the transmembrane region, such amino acid sequence having 60% homology or higher to the amino acid sequence in the transmembrane region of the Y2 receptor shown in Figure 11.
67. A method of claim 66 wherein the Y2 receptor is a human Y2 receptor.
68. A method of claim 66 wherein the Y2 receptor is a rat Y2 receptor.
69. A method for determining whether a ligand can bind specifically to a Y2 receptor which comprises

preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the cell extract, contacting the ligand with the membrane fraction under conditions permitting binding of ligands to such receptor, and detecting the presence of any ligand bound to the Y2 receptor, thereby determining whether the compound is capable of specifically binding to a Y2 receptor.

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70. A method of claim 69 wherein the Y2 receptor is a human Y2 receptor.

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71. A method of claim 69 wherein the Y2 receptor is a rat Y2 receptor.

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72. A method of any of claims 63, 64, 65, 66, 67, 68, 69, 70, or 71 wherein the ligand is not previously known.

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73. A ligand determined by the method of claim 72.

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74. A method for determining whether a ligand is a Y2 receptor agonist which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with the ligand under conditions permitting the activation of a functional Y2 receptor response from the cell, and detecting by means of a bioassay, such as a second messenger assay, an increase in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor agonist.

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75. A method for determining whether a ligand is a Y2 receptor agonist which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a

membrane fraction from the cell extract, contacting the membrane fraction of the extract with the ligand under conditions permitting the activation of a functional Y2 receptor response, and detecting by means of a bioassay, such as a second messenger assay, an increase in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor agonist.

76. A method of either of claims 74 or 75 wherein the Y2 receptor is a human Y2 receptor.

77. A method of either of claims 74 or 75 wherein the Y2 receptor is a rat Y2 receptor.

78. A method for determining whether a ligand is a Y2 receptor antagonist which comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with the ligand in the presence of a known Y2 receptor agonist, such as NPY, under conditions permitting the activation of a functional Y2 receptor response, and detecting by means of a bioassay, such as a second messenger assay, a decrease in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor antagonist.

79. A method for determining whether a ligand is a Y2 receptor antagonist which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction of the extract with the ligand in the presence of a known Y2 receptor agonist, such as NPY, under conditions permitting the activation of a functional Y2 receptor response, and detecting by means of a bioassay, such as a second messenger

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assay, a decrease in Y2 receptor activity, thereby determining whether the ligand is a Y2 receptor antagonist.

- 5 80. A method of either of claims 78 or 79 wherein the Y2 receptor is a human Y2 receptor.
81. A method of either of claims 78 or 79 wherein the Y2 receptor is a rat Y2 receptor.
- 10 82. A method of any of claims 74, 75, 78, or 79 wherein the second messenger assay comprises measurement of intracellular cAMP.
- 15 83. A method of any of claims 74, 75, 78, or 79 wherein the second messenger assay comprises measurement of intracellular calcium mobilization.
- 20 84. A method of any of claims 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, or 81 wherein the cell is a mammalian cell.
- 25 85. A method of claim 84 wherein the mammalian cell is nonneuronal in origin.
- 30 86. A method of claim 85, wherein the mammalian cell is nonneuronal in origin is a COS-7 cell.
- 35 87. A method of claim 85, wherein the mammalian cell nonneuronal in origin is a 293 human embryonic kidney cell.
88. The cell of claim 87 designated 293-hY2-10 (ATCC Accession No. 11837).
89. A method of claim 85, wherein the mammalian cell nonneuronal in origin is a LM(tk-) cell.

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90. A method of claim 85, wherein the mammalian cell nonneuronal in origin is a NIH-3T3 cell.
- 5 91. A cell of claim 90 designated N-hY2-5 (ATCC Accession No. CRL-11825).
92. A ligand detected by the method of any of claims 74, 75, 76, 77, 78, 79, 80, or 81.
- 10 93. A ligand of claim 92 wherein the ligand is not previously known.
94. A pharmaceutical composition comprising an amount of a Y2 receptor agonist determined by the method of
15 either of claims 74 or 75 effective to activate a Y2 receptor and a pharmaceutically acceptable carrier.
95. A pharmaceutical composition of claim 94 wherein the Y2 receptor agonist is not previously known.
20
96. A pharmaceutical composition which comprises an amount of a Y2 receptor antagonist determined by the method of either of claims 78 or 79 effective to decrease activity of a Y2 receptor and a
25 pharmaceutically acceptable carrier.
97. A pharmaceutical composition of claim 96 wherein the Y2 receptor antagonist is not previously known.
- 30 98. A method of screening drugs to identify drugs which specifically bind to a Y2 receptor on the surface of a cell which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs under conditions
35 permitting binding of drugs to the Y2 receptor, and determining those drugs which bind specifically to the transfected cell, thereby identifying drugs

which bind specifically to a Y2 receptor.

- 5 99. A method of screening drugs to identify drugs which bind specifically to a Y2 receptor on the surface of a cell which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction with a plurality of drugs under conditions permitting binding of drugs to the Y2 receptor, and determining those drugs which bind specifically to the transfected cell, thereby identifying drugs which bind specifically to a Y2 receptor.
- 10 100. A method of either of claims 98 or 99 wherein the Y2 receptor is a human Y2 receptor.
- 15 101. A method of either of claims 98 or 99 wherein the Y2 receptor is a rat Y2 receptor.
- 20 102. A method of screening drugs to identify drugs which act as agonists of a Y2 receptor which comprises contacting a cell transfected with and expressing nucleic acid encoding the Y2 receptor with a plurality of drugs under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which activate such receptor using a bioassay, such as a second messenger assay, thereby identifying drugs which act as agonists of a Y2 receptor.
- 25 103. A method of screening drugs to identify drugs which act as agonists of a Y2 receptor which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the
- 30
- 35

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- cell extract, contacting the membrane fraction with a plurality of drugs under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which activate such receptor using a bioassay, such as a second messenger assay, thereby identifying drugs which act as agonists of a Y2 receptor.
104. A method of either of claims 102 or 103 wherein the Y2 receptor is a human Y2 receptor.
105. A method of either of claims 102 or 103 wherein the Y2 receptor is a rat Y2 receptor.
106. A method of screening drugs to identify drugs which act as antagonists of Y2 receptors which comprises contacting a cell transfected with and expressing nucleic acid encoding a Y2 receptor with a plurality of drugs in the presence of a known Y2 receptor agonist such as NPY under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which inhibit the activation of the receptor using a bioassay, such as a second messenger assay, thereby identifying drugs which act as antagonists of Y2 receptors.
107. A method of screening drugs to identify drugs which act as antagonists of Y2 receptors which comprises preparing a cell extract from cells transfected with and expressing nucleic acid encoding the Y2 receptor, isolating a membrane fraction from the cell extract, contacting the membrane fraction with a plurality of drugs in the presence of a known Y2 receptor agonist such as NPY under conditions permitting the activation of a functional Y2 receptor response, and determining those drugs which inhibit the activation of the receptor using a

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bioassay, such as a second messenger assay, thereby identifying drugs which act as antagonists of Y2 receptors.

- 5 108. A method of either of claims 106 or 107 wherein the Y2 receptor is a human Y2 receptor.
109. A method of either of claims 106 or 107 wherein the Y2 receptor is a rat Y2 receptor.
- 10 110. A method of any of claims 102, 103, 106 or 107 wherein the second messenger assay comprises measurement of intracellular cAMP.
- 15 111. A method of any of claims 102, 103, 106, or 107 wherein the second messenger assay comprises measurement of intracellular calcium mobilization.
- 20 112. A method of any of claims 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, or 109 wherein the cell is a mammalian cell.
- 25 113. A method of claim 112 wherein the mammalian cell is nonneuronal in origin.
- 30 114. The method of claim 113 wherein the mammalian cell nonneuronal in origin is a Cos-7 cell.
115. The method of claim 113 wherein the mammalian cell nonneuronal in origin is a 293 human embryonic kidney cell.
- 35 116. The cell of claim 115 designated 293-hY2-10 (ATCC Accession No. 11837).
117. The method of claim 113 wherein the mammalian cell nonneuronal in origin is a LM(tk-) cell.

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118. The method of claim 113 wherein the mammalian cell nonneuronal in origin is a NIH-3T3 cell.
119. The cell of claim 118 designated N-hY2-5 (ATCC Accession No. CRL-11825).
120. A pharmaceutical composition comprising an effective amount of a drug identified by the method of either of claims 102 or 103 and a pharmaceutically acceptable carrier.
121. A pharmaceutical composition comprising an effective amount of a drug identified by the method of either of claims 106 or 107 and a pharmaceutically acceptable carrier.
122. A method of detecting expression of a Y2 receptor by a cell by detecting the presence of mRNA coding for a Y2 receptor which comprises obtaining total mRNA from the cell and contacting the mRNA so obtained with the nucleic acid probe of claim 39 under hybridizing conditions, and detecting the presence of mRNA hybridized to the probe, thereby detecting the expression of Y2 receptor by the cell.
123. A method of treating an abnormality in a subject, wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering to a subject an effective amount of the pharmaceutical composition of either of claims 94 or 120, thereby treating the abnormality.
124. A method of treating an abnormality in a subject, wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering to a subject an effective amount of Y2 receptor agonist determined by any of claims 74, 75, 102, or 103,

thereby treating the abnormality.

- 5 125. A method of treating an abnormality in a subject,
 wherein the abnormality is alleviated by decreasing
 the activity of a Y2 receptor which comprises
 administering to a subject an effective amount of
 the pharmaceutical composition of either of claims
 96 or 121, thereby treating the abnormality.
- 10 126. A method of treating an abnormality in a subject,
 wherein the abnormality is alleviated by decreasing
 the activity of a Y2 receptor which comprises
 administering to the subject an effective amount of
15 a Y2 receptor antagonist determined by the methods
 of any of claims 78, 79, 106, or 107, thereby
 treating the abnormality.
- 20 127. The method of either of claims 125 or 126 wherein
 the abnormality is a cognitive disorder.
128. The method of either of claims 125 or 126 wherein
 the abnormality is a gastrointestinal disorder.
- 25 129. The method of either of claims 125 or 126 wherein
 the abnormality is sleeping disorder.
130. The method of either of claims 125 or 126 wherein
 the abnormality is epilepsy.
- 30 131. The method of either claims 125 or 126 wherein the
 abnormality is hypertension.
132. The method of either of claims 123 or 124 wherein
 the abnormality is memory loss.
- 35 133. The method of either of claims 123 or 124 wherein
 the abnormality is diarrhea.

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134. The method of either of claims 123 or 124 wherein the abnormality is nasal congestion.
- 5 135. The method of either of claims 123 or 124 wherein the abnormality is pain.
- 10 136. A method of treating an abnormality in a subject, wherein the abnormality alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an amount of the pharmaceutical composition of claim 56 effective to block binding of ligands to the Y2 receptor, thereby treating the abnormality.
- 15 137. A method of treating an abnormality in a subject, wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an effective amount of the pharmaceutical composition of claim 51, thereby
- 20 treating the abnormality.
138. The method of either of claims 136 or 137 wherein the abnormality is a cognitive disorder.
- 25 139. The method of either of claims 136 or 137 wherein the abnormality is a gastrointestinal disorder.
140. The method of either of claims 136 or 137 wherein the abnormality is epilepsy.
- 30 141. The method of either of claims 136 or 137 wherein the abnormality is hypertension.
142. The method of either of claims 136 or 137 wherein
- 35 the abnormality is sleeping disorder.
143. A method of detecting the presence of a Y2 receptor

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on the surface of a cell which comprises contacting the cell with the antibody of claim 46 under conditions permitting binding of the antibody to the receptor, and detecting the presence of the antibody bound to the cell, thereby detecting the presence of a Y2 receptor on the surface of the cell.

144. A method of determining the physiological effects of expressing varying levels of Y2 receptors which comprises producing a transgenic nonhuman mammal of claim 55 whose levels of human Y2 receptor expression are varied by use of an inducible promoter which regulates Y2 receptor expression.

145. A method of determining the physiological effects of expressing varying levels of Y2 receptors which comprises producing a panel of transgenic nonhuman mammals of claim 55 each expressing a different amount of Y2 receptor.

146. A method for identifying a Y2 receptor antagonist capable of alleviating an abnormality in a subject, wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor which comprises administering the antagonist to a transgenic nonhuman mammal of any of claims 57, 58, or 59 and determining whether the antagonist alleviates the physical and behavioral abnormalities displayed by the transgenic nonhuman mammal as a result of activity of a Y2 receptor, thereby identifying a Y2 antagonist.

147. An antagonist identified by the method of claim 146.

148. A pharmaceutical composition comprising an effective amount of an antagonist identified by the method of claim 146 and a pharmaceutically acceptable carrier.

149. A method for treating an abnormality in a subject wherein the abnormality is alleviated by decreasing the activity of a Y2 receptor which comprises administering to the subject an effective amount of the pharmaceutical composition of claim 148, thereby treating the abnormality.
150. A method for identifying a Y2 receptor agonist capable of alleviating an abnormality wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering the agonist to the transgenic nonhuman mammal of any of claims 57, 58, or 59 and determining whether the agonist alleviates the physical and behavioral abnormalities displayed by the transgenic nonhuman mammal, thereby identifying a Y4 receptor agonist.
151. An agonist identified by the method of claim 150.
152. A pharmaceutical composition comprising an effective amount of an agonist identified by the method of claim 150 and a pharmaceutically acceptable carrier.
153. A method for treating an abnormality in a subject wherein the abnormality is alleviated by activation of a Y2 receptor which comprises administering to the subject an effective amount of the pharmaceutical composition of claim 152, thereby treating the abnormality.
154. A method for diagnosing a predisposition to a disorder associated with the activity of a specific Y2 receptor allele which comprises:
- obtaining nucleic acid of subjects

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suffering from the disorder;

- 5 b. performing a restriction digest of the
 nucleic acid with a panel of
 restriction enzymes;
- 10 c. electrophoretically separating the
 resulting nucleic acid fragments on a
 sizing gel;
- 15 d. contacting the resulting gel with a
 nucleic acid probe capable of
 specifically hybridizing to nucleic
 acid encoding a Y2 receptor and
 labelled with a detectable marker;
- 20 e. detecting labelled bands which have
 hybridized to the nucleic acid encoding
 a Y2 receptor labelled with a
 detectable marker to create a unique
 band pattern specific to the nucleic
 acid of subjects suffering from the
 disorder;
- 25 f. preparing nucleic acid obtained for
 diagnosis by steps a-e; and
- 30 g. comparing the unique band pattern
 specific to the nucleic acid of
 subjects suffering from the disorder
 from step e and the nucleic acid
 obtained for diagnosis from step f to
 determine whether the patterns are the
 same or different and to diagnose
35 thereby predisposition to the disorder
 if the patterns are the same.

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155. The method of claim 154 wherein a disorder associated with the expression of a specific Y2 receptor allele is diagnosed.

5 156. A method of preparing the isolated, purified Y2 receptor of claim 15 which comprises:

- 10 a. constructing a vector adapted for expression in a cell which comprises the regulatory elements necessary for the expression of nucleic acid in the cell operatively linked to the nucleic acid encoding a Y2 receptor as to permit expression thereof, wherein the cell is selected from the group consisting of bacterial cells, yeast cells, insect cells and mammalian cells;
- 15
- 20 b. inserting the vector of step (a) in a suitable host cell;
- c. incubating the cells of step (b) under conditions allowing the expression of a Y2'receptor;
- 25
- d. recovering the receptor so produced;
- e. purifying the receptor so recovered.
- 30

[illegible]

[illegible]

1002 ATGGGTCCAATAGGTGCAGAGGCTGATGAGAACCAAGACAGTGGAGAAAT 1051
 197ATGAATTCAACATTATTTC 216
 1052 GAAGGTGGAACAATAACGGGCCACAACAACCTCCTAGAGGTGAAGTGTCC 1101
 217 CCAGGTTGAAAAATCATTCAGTCCCACTCTAATTCTCTCAGAGAAGAAATGCC 266
 1102 CTGACCCCTGAGCCAGAGCTTATAGATAGTACCAAGCTGATGAGGTACAA 1151
 267 AGCTTCTGGCTTTTGAAAAATGATGATTGTCTCATCTGCCCTTGGCCATGATA 316
 1152 GTTGTCTCATATTGGCCCTACTGCTCCATCATCTTGCTTGGGGTAATTGG 1201
 317 TTTACCTTAGCTCTTGCTTATGGAGCTGTGATCATCTTGGTGTCTCTGG 366
 1202 CAACTCCTTGGTGATCCATGTGGTGATCAAAATTCAAAGAGCATGCGCACAG 1251
 367 AAACCTGGCCCTTGATCATATAATCATCTTGAAAAACAAAAGGAGATGAGAAATG 416
 1252 TAACCAACTTTTTCATTTGCCAATCTGGCTGTGGCAGATCTTTTGGTGAAC 1301
 417 TTACCAACAATCCTGTATTGTGAACCTTTCTCTTCTCAGACTTGGCTTGTGGCC 466

1302 ACTCTGTGTCACCGTTCACTCTTACCTATACCTTAATGGGGAGTGGA 1351
| | | | | | | | | | | | | | | | | |
467 ATCATGTGTCCTCCCTTTACATTGTGCTACACATTAAATGGACCACCTGGGT 516

1352 AATGGGTCTCTGTGCCACCTGGTGCCCTATGCCCCAGGGCCTGGCAG 1401
| | | | | | | | | | | | | | | | | |
517 CTTTGGTGAGGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAA 566

1402 TACAAGTATCCACAATCACCTTTGACAGTAATTGCCCTGGACCGGCACAGG 1451
| | | | | | | | | | | | | | | | | |
567 TCACGTGTCCATTTTCTCTCTGTTCTCATTGCTGTGGAACGACATCAG 616

1452 TGCCATCGTCTACCACTTAGAGAGCAAGATCTCCAAGCGAATCAGCTTCCT 1501
| | | | | | | | | | | | | | | | | |
617 CTGATAATCAACCCTCGAGGTGGAGACCAAAATAATAGACATGCTTATGT 666

1502 GATTATTGGCTTGGCCTGGGGCATCAGTGCCCCCTGCTGGCAAGTCCCCCTGG 1551
| | | | | | | | | | | | | | | | | |
667 AGGTATTGCTGTGATTGGGTCTCTGCTG..TGGCTTCTTCTTTGCCCCTTT 714

1552 CCATCTTCCGGGAGTATTCGCTGATTGAGATCATCCCGGACTTTTGAGATT 1601
| | | | | | | | | | | | | | | | | |
715 CCTGATCTACCAAGTAATGACTGA.TGAGCCGTTTCCAAAAATGTAACACTT 763

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FIGURE 3C

1602 GTGGCCCTGTACTGAAAAGTGGCCTGGCGAGGAGAA.....GAGCAT 1642
| | | | | | | | | | | | | | | | | | | | | |
764 GATGCGTACAAAGACAAATACGTGCTTTGATCAATTTCATCGGACTC 813
| | | | | | | | | | | | | | | | | | | | | |
1643 CTATGGCACTGTCTATAGTCTTTCTTCTTGTGATCTTGTATGTTTGC 1692
| | | | | | | | | | | | | | | | | | | | | |
814 TCATAGGTTGCTTATACCACTCTCCTCTTGGTCTGCAGTATTTTGGTC 863
| | | | | | | | | | | | | | | | | | | | | |
1693 CTCGGGCATTATATCATTTTCCCTACACTCGCATTT.....GGAGTA 1734
| | | | | | | | | | | | | | | | | | | | | |
864 CACTTTGTTTATATTTATTTGCTACTTCAAGATATATACGCCATAAAA 913
| | | | | | | | | | | | | | | | | | | | | |
1735 AATTGAAGAACCATGTCAGTCCCTGGAGCTGCAAAATGACCACCTACCATCAG 1784
| | | | | | | | | | | | | | | | | | | | | |
914 AGGAGAAACAACATGATGGACAAGATGAGAGACAATAAGTACAGGTCCAG 963
| | | | | | | | | | | | | | | | | | | | | |
1785 CGAAGGCAAAA.AACCACCAAAATGCTGGTGTGTGGTGGTGGTGTG 1833
| | | | | | | | | | | | | | | | | | | | | |
964 TGAACCAAAAAGAAATCAATATCATGCTGCTCTCCATTGTGGTAGCATTTG 1013
| | | | | | | | | | | | | | | | | | | | | |
1834 CGGTCAGCTGGCTGCCCTCTCCATGCCCTTCCAGCTTGCCCGTTGACATTGAC 1883
| | | | | | | | | | | | | | | | | | | | | |
1014 CAGTCTGCTGGCTCCCTCTTACCATCTTTAAACACACTGTGTGTTGATTGGAAT 1063
| | | | | | | | | | | | | | | | | | | | | |

1884 AGCCAGGTCCTGGACCTGAAGGAGTACAAACTCATCTTCAAGTGTCCA 1933
 11064 CATCAGATCATTGCTACCTGCAACCACAATCTGTTATTCTCTGCTCTGCCA 1113
 1934 CATCATCGCCATGTGCTCCACTTTTGCCCAATCCCTTCTCTATGGCTGGA 1983
 11114 CCTCACAGCAATGATATCCACTTGTGTCAACCCCATATTTATGGGTTCC 1163
 1984 TGAACAGCAACTACAGAAAGGCTTTCTCTCTCGGCCTTCCGC...TGTGAG 2030
 11164 TGAACAAAAAAGCTTCCAGAGAGACTTGCAGTTCTTCTTCAACTTTTGTGAT 1213
 2031 CAGCGGTTGGATGCCATTCACTCTGAGGTGTCCGTGACATTCAAG... 2075
 1214 TTCCGGTCTCGGGATGATGATTATGAAACAATAGCCATGTCCACGATGCA 1263
 2076GCTAAAAAGAACCTGGAGGTCAGAAAGAACAGTGGC.CCCA 2115
 1264 CACAGATGTTTCCAAAACTTCTTTGAAGCAAGCAAGCCAGTCGCATTTA 1313
 2116 ATGACTCTTTCACAGAGGCTACCAATGTCTAA..... 2147
 1314 AAAAAATCAACAACAATGATGATGATAATGAAAAAATCTGA 1351

FIGURE 4A

FIGURE 4A
FIGURE 4B

```

1  MGPIGAEDENQTVEMKVEQYGPQTTPRGELVPDPEPELIDSTKLEI VQ 50
   |... ..||:|. .:::.....:| |: ::
1  MNSTLFSQVENHSVH...SNFSEKNAQLLAFEND.....DCHLPLAMI 40

51  VVLILAYCSIILLGVIGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVN 100
   ..| |||...:| || :| ::| |.|||:|.||...|||.
41  FTLALAYGAVIILGVSGNLALIIILKQKEMRNVTNIIIVNLSFSDLVA 90

101  TLCPLFTLTYTLMGEWKMGPVLC HLPYAQGLAVQVSTITLTVTIALDRHR 150
   .:|||||:..|||:| :|...:| |:..:| |:..:| |:..:|
91  IMCLPFTFVYTLMDHWVFGCEAMCKLNPVFVQCVSITVSIFSLVLI AVERHQ 140

151  CIVYHLESKISRISFLIIGLAWGISALLASPLAIFREYSLIEIIPDFEI 200
   |: .:..:..| :.:| |:| :.:| |:| :.:| |:| :.:|
141  LIINPRGWRPNRHRAYVGVIAVIWVLAVASSLPFLIYQVMT.DEPFQNVTL 189

```


FIGURE 4B

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201 VACTEKW.....PGEKSIYGTVYSLSSLLILYVLPPLGIISFSYTRIW 243
   |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
190 DAYKDYVCFDQFPSPDSHRLSYTLL...LVLYFGPLCFIFICYFKIY 235
   |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
244 SKLK..NHVSPGAANDHYHQRRQKTK.MLVCVVVVFVAVSWLPLHAFQLA 290
   :|| |:: |::|: |::|: |::|: |::|: |::|: |::|:
236 IRLKRRNNMMDKMRDNKYRSSETKRINIMLSIVVAFVAVCWLPPLTIFNTV 285
   |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
291 VDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPLLYGWMNSNYRKAF.... 336
   .|: |:: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
286 FDWNHQIATCNHNLLFLCHLTAMISTCVNPIFYGFLNKNFQRDLQFFF 335
   |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
337 .LSAFRCQR.....LDAIHSEVSVT.FKAKKNLEVRK..NSGPNDSFT 376
   ::||: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
336 NFCDFRSRDDDYEIAMSTMHTDVSKTSLKQASPVAFKKINNNDNEKI* 385
   |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
377 EATNV* 381

```

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FIGURE 5A

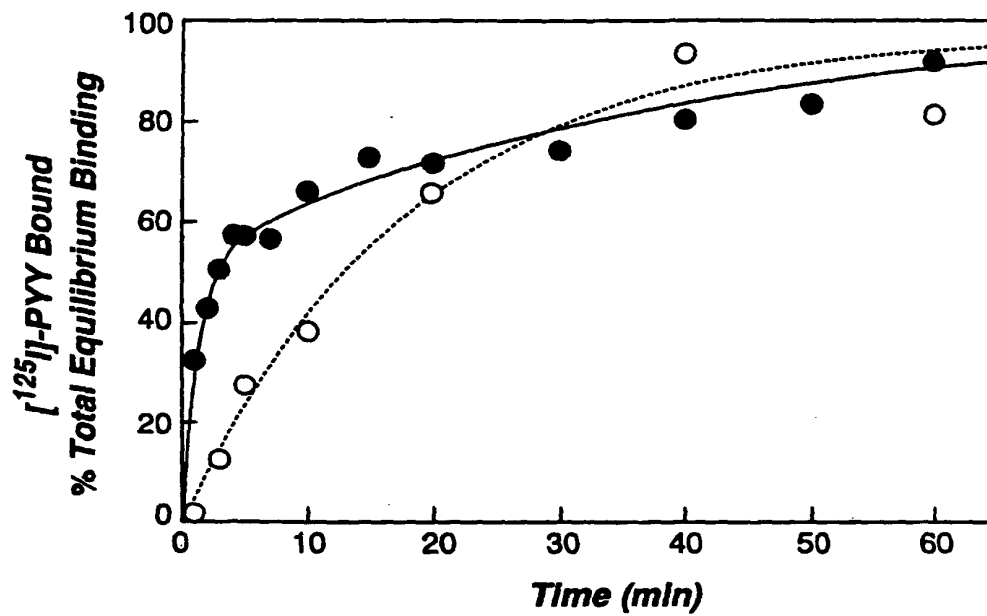
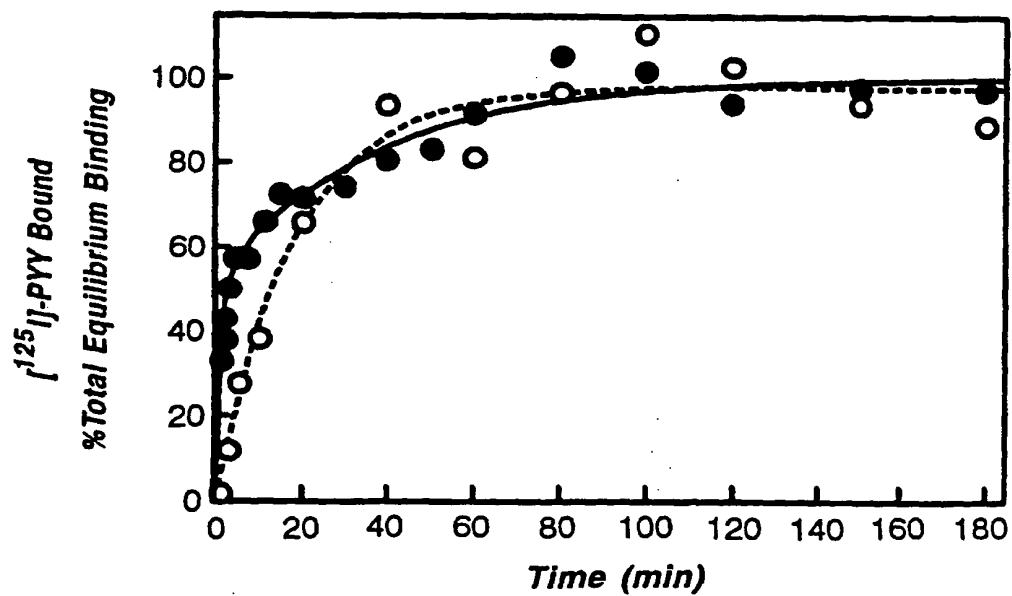
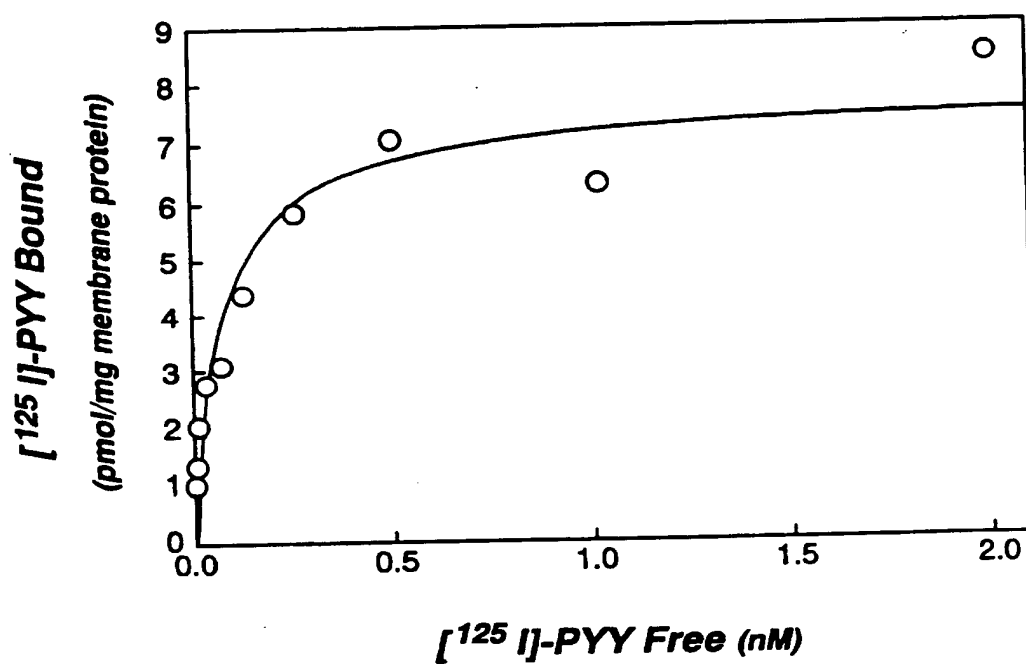


FIGURE 5B



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FIGURE 6



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FIGURE 7A

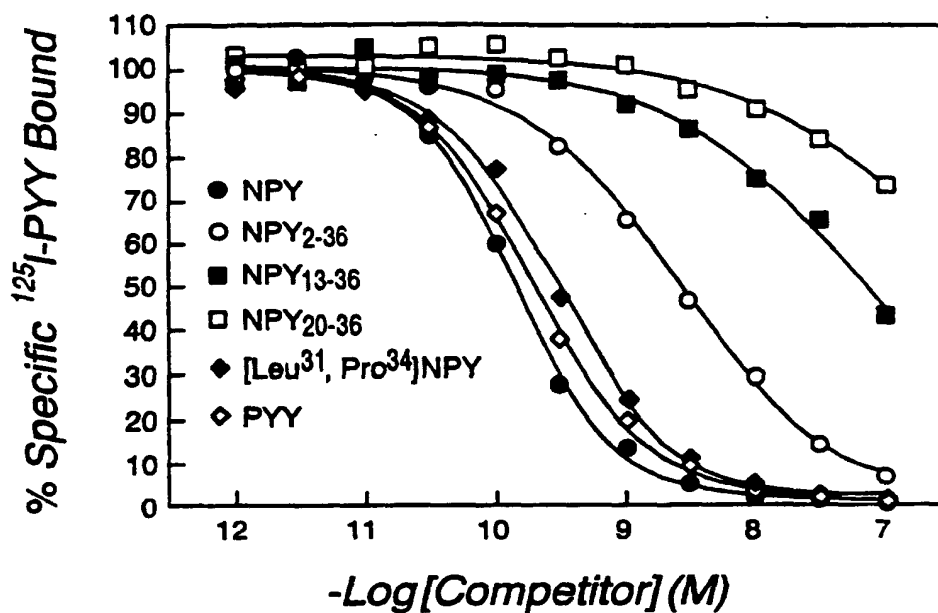


FIGURE 7B

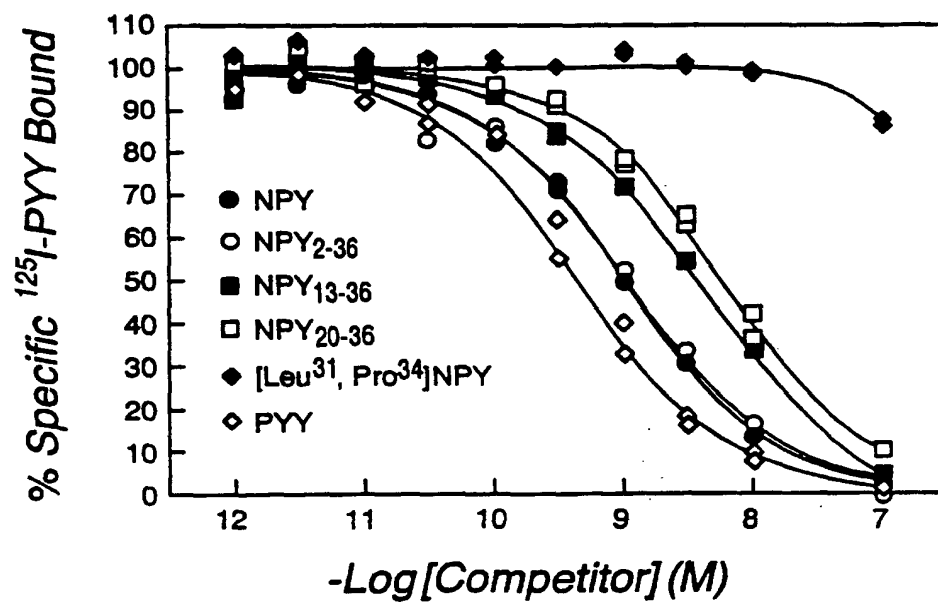


FIGURE 8A

FIGURE 8A
FIGURE 8B
FIGURE 8C
FIGURE 8D
FIGURE 8E

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-200      -180      -160
.          .          .
GTTGTTAAACAGACTCGTGTAAGGATTGCTTTATGGAGCTTTTATGAGATCTGTGGTGT

-140      -120      -100
.          .          .
GATGAATCAGAACACAGCTACGCAGAGGAGCTCAGCCTAAACTAAATCAACCCCTTAGG

-80      -60      -40
.          .          .
ATGGTTCCTCTGTTTCACTAACTTTTTTTTAAATGTCGTTTTCTGTATAGATTCTTGTGCTA

-20      1      20
.          .          .
TCTGCAGGCCAAATTGGAACTGAGGTGAAGATGGGCCCATTAGGTGCAGAGGCAGATGAG
      M G P L G A E A D E

40      60      80
.          .          .
AATCAAACCTGTAGAAGTGAAAGTGGAACCTCTATGGTCGGGGCCCACTCCTAGAGGT
N Q T V E V K V E L Y G S G P T T P R G

```

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FIGURE 8B

100 120 140
GAGTGGCCCCCTGATCCAGAGCCGGAGCTCATAGACAGCACCAAACTGGTTGAGGTGCAG
E L P P D P E P E L I D S T K L V E V Q

160 180 200
GTGGTCCCTTATACTGGCCTATTGTTCCATCATCTTGCTGGCGTAGTTGGCAACTCTCTG
V V L I L A Y C S I I L L G V V G N S L

220 240 260
GTAATCCATGTGGTGATCAAATTCAAGAGCATGCGCACAGTAACCAACTTTTATTGCCC
V I H V V I K F K S M R T V T N F F I A

280 300 320
AACCTGGCTGTGGCGGATCTTTTGGTGAACACACCCTGTGCGCTGCCATTCACTCTTACCTAT
N L A V A D L L V N T L C L P F T L T Y

340 360 380
ACCTTGATGGGGAGTGGAATAATGGGTCCAGTTTGTGCCATTGTTGGTGCCTATGCCCCAG
T L M G E W K M G P V L C H L V P Y A Q

400 420 440
 GGTCTGGCAGTACAAGTGTCCACAATAACTTTGACAGTCATTGCTTTGGACCGACATCGT
 G L A V Q V S T I T L T V I A L D R H R
 460 480 500
 TGCATTGTCTACCACTGGAGAGCAAGATCTCCAAGCAAATCAGCTTCTCGATTATTGGC
 C I V Y H L E S K I S K Q I S F L I I G
 520 540 560
 CTGGCGTGGGTGTACGCGTCTGTGGCAAGTCCCTTGCCATCTTCCGGGAGTACTCA
 L A W G V S A L L A S P L A I F R E Y S
 580 600 620
 CTGATTGAGATTATTCTGACTTTGAGATTGTAGCCTGTACTGAGAAATGCCCGGGGAG
 L I E I I P D F E I V A C T E K W P G E
 640 660 680
 GAGAAGAGTGTGTACGGTACAGTCTACAGCCTTCCACCCCTGCTAATCCTCTACGTTTGG
 E K S V Y G T V Y S L S T L L I L Y V L

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FIGURE 8D

700		720		740
CCTCTGGGCATCATATCTTTCTCTACACCCGGATCTGGAGTAAGCTAAAGAACCACGTT				
P L G I I S F S Y T R I W S K L K N H V				
760		780		800
AGTCCTGGAGCTGCAAGTGACCATTAACCATCAGCGAAGGCACAAACGACCAAAATGCTC				
S P G A A S D H Y H Q R R H K T T K M L				
820		840		860
GTGTGCGTGGTAGTGGTGTTCAGTCAGCTGGCTGCCCTCCATGCCCTTCCAACCTTGCT				
V C V V V V F A V S W L P L H A F Q L A				
880		900		920
GTGGACATCGACAGCCATGTCCTGGACCTGAAGGAGTACAAACTCATCTTCACCGTGTTT				
V D I D S H V L D L K E Y K L I F T V F				
940		960		980
CACATTATTGCGATGTGCTCCACCTTCGCCCAACCCCTTCTCTATGGCTGGATGAACAGC				
H I I A M C S T F A N P L L Y G W M N S				

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FIGURE 8E

1000 1020 1040
A A C T A C A G A A A G C T T T C C T C T C A G C C T T C C G C T G T G A C A G A G G T T G G A T G C C A T T C A C
N Y R K A F L S A F R C E Q R L D A I H

1060 1080 1100
T C G G A G G T G T C C A T G A C C T T C A A G G C T A A A A G A A C C T G G A A G T C A A A A G A A C A A T G G C
S E V S M T F K A K K N L E V K K N N G

1120 1140 1160
C T C A C T G A C T C T T T T C A G A G G C C A C C A C G T G T A A G A A T G C T G T G A A A G T A C G T G G G T A
L T D S F S E A T N V *

1180 1200 1220
A A T T G C G A C C A G A G T T G C C A A C C T G G T T A G G G A A G G T T T T C T G G C T A G T G C A T G C C A C C T

1240 1260 1280
C C C A T T G T A T T G A C C C T A A A A G C A T C A G A G T G G A A G C C C C A G C G G T A T T G T T C C T G G A A A

1300 1320 1340
A C T G G C T G G A A G A A T G A G G A G A A A T A A A C A G A T T G C T G T G G C G C A A C G T T C T G A T

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FIGURE 9A

FIGURE 9A
FIGURE 9B
FIGURE 9C
FIGURE 9D

```

-50          -30          -10          1
TTTCTGTTATAGATTCTTGTGCTATCTGCAGGCCAAATTGGAACCTGAGGTGAAGATGGGC
M G

10          30          50
CCATTAGGTGCAGAGGCAGATGAGAATCAAACCTGTAGAAGTGAAAGTGGAAATTCTATGGG
P L G A E A D E N Q T V E V K V E F Y G

70          90          110
TCGGGGCCCAACCACTCCTAGAGGTGAGTTGCCCCCTGATCCAGAGCCGGAGCTCATAGAC
S G P T T P R G E L P P D P E P E L I D

130         150         170
AGCACCAAACTGGTTGAGGTGCAGGTGGTGCTTATACTGCGCTATTGTTCCATCATCTTG
S T K L V E V Q V V L I L A Y C S I I L

190         210         230
CTGGGCGTAGTTGGCAACTCTCTGGTAATCCATGTGGTGATCAAAATTCAAGAGCATCGGC
L G V V G N S L V I H V V I K F K S M R

```

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FIGURE 9B

250 270 290
ACAGTAACCAACTTTTATTGCCAAACCTGGCTGTGGCGGATCTTTTGGTGAACACCCCTG
T V T N F F I A N L A V A D L L V N T L
310 330 350
TGCCTGCCATTCACTCTTACCTATACCTTGATGGGGAGTGGAATAATGGGTCCAGTTTGG
C L P F T L T Y T L M G E W K M G P V L
370 390 410
TGCCATTGGTGCCCTATGCCCAGGGTCTGGCAGTACAAGTGTCCACAATAACTTTGACA
C H L V P Y A Q G G L A V Q V S T I T L T
430 450 470
GTCATTGCTTTGGACCGACATCGTTGCATTGTCTACCACCTGGAGAGCAAGATCTCCAAG
V I A L D R H R C I V Y H L E S K I S K
490 510 530
CAAATCAGCTTCCTGATTATTGGCCGTGGCGTGGGTGTCAGCGCTCTGCTGGCAAGTCCC
Q I S F L I I G L A W G V S A L L A S P

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FIGURE 9C

550 570 590
CTTGCCATCTTCGGGAGTACTCACTGATTGAGATTATTCCTGACTTTGAGATTGTAGCC
L A I F R E Y S L I E I I P D F E I V A

610 630 650
TGTA CTGAGAAATGGCCCGGGAGGAGAAGAGTGTACGGTACAGCTACAGCCTTTCC
C T E K W P G E E K S V Y G T V Y S L S

670 690 710
ACCCTGCTAATCCTCTACGTTTGGCCCTCTGGGCATCATATCTTCTCCTACACCCGGATC
T L L I L Y V L P L G I I S F S Y T R I

730 750 770
TGGAGTAAGCTAAAGAACCACGTTAGTCCTGGAGCTGCAAGTGACCATTAACCATCAGCGA
W S K L K N H V S P G A A S D H Y H Q R

790 810 830
AGGCACAAAATGACCAAAAATGCTCGTGGTGGTAGTGGTGTTCAGTCAGCTGGCTG
R H K M T K M L V C V V V F A V S W L

850	870	890
CCCCTCCATGCCTTCCAACTTGCTGTGGACATCGACAGCCATGTCTCGACCTGAAGGAG		
P L H A F Q L A V D I D S H V L D L K E		
910	930	950
TACAAACTCATCTTCACCGTGTTCACACATTATTGCGATGTGCTCCACCTTCGCCAACCCCC		
Y K L I F T V F H I I A M C S T F A N P		
970	990	1010
CTTCTCTATGGCTGGATGAACAGCAACTACAGAAAGCTTTCCTCTCAGCCTTCCGCTGT		
L L Y G W M N S N Y R K A F L S A F R C		
1030	1050	1070
GAGCAGAGGTGGATGCCATTCACTCGGAGGTGTCCATGACCTTCAAGGCTAAAAAGAAC		
E Q R L D A I H S E V S M T F K A K K N		
1090	1110	1130
CTGGAAGTCAAAAAGAACAATGGCCTCACTGACTCTTTTTCAGAGGCCACCAACGTGTAA		
L E V K K N N G L T D S F S E A T N V *		

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FIGURE 10A

FIGURE 10A
FIGURE 10B
FIGURE 10C
FIGURE 10D

Hum Y2	ATGGGTCCAATAGGTGCAGAGGCTGATGAGAACACAGACAGTGGAAGAAAT	50
Rat Y2a	ATGGGCCCCATTAGGTGCAGAGGCAGATGAGAAATCAAACCTGTAGAAAGTGAA	50
Rat Y2b	ATGGGCCCCATTAGGTGCAGAGGCAGATGAGAAATCAAACCTGTAGAAAGTGAA	50
Hum Y2	GAAGGTGGAAACAATACGGGGCCACAACAACCTCCTAGAGGTGAACCTGGTCC	100
Rat Y2a	AGTGGAAGTCTATGGTGGGGCCCCACCACCTCCTAGAGGTGAGTTGCCCC	100
Rat Y2b	AGTGGAAGTCTATGGTGGGGCCCCACCACCTCCTAGAGGTGAGTTGCCCC	100
Hum Y2	CTGACCCCTGAGCCAGAGCTTATAGATAGTACCAAGCTGATTGAGGTACAA	150
Rat Y2a	CTGATCCAGAGCCGGAGCTCATAGACAGCACCAAACTGGTTGAGGTGCAG	150
Rat Y2b	CTGATCCAGAGCCGGAGCTCATAGACAGCACCAAACTGGTTGAGGTGCAG	150
Hum Y2	GTGTGTTCTCATATTGGCCCTACTGCTCCATCATCTTGCTTGGGGTAATTGG	200
Rat Y2a	GTGGTCCTTATACCTGGCCCTATTGTTCCATCATCTTGCTGGCGGTAGTTGG	200
Rat Y2b	GTGGTCCTTATACCTGGCCCTATTGTTCCATCATCTTGCTGGCGGTAGTTGG	200
Hum Y2	CAACTCCTTGGTGATCCATGTGGTGATCAAATTCAGAGCATGCGCACAG	250
Rat Y2a	CAACTCTCTGGTAATCCATGTGGTGATCAAATTCAGAGCATGCGCACAG	250
Rat Y2b	CAACTCTCTGGTAATCCATGTGGTGATCAAATTCAGAGCATGCGCACAG	250
Hum Y2	TAACCAACTTTTTCATTGCCAATCTGGCTGTGGCAGATCTTTTGGTGAAC	300
Rat Y2a	TAACCAACTTTTTCATTGCCAATCTGGCTGTGGCAGATCTTTTGGTGAAC	300
Rat Y2b	TAACCAACTTTTTCATTGCCAATCTGGCTGTGGCAGATCTTTTGGTGAAC	300
Hum Y2	ACTCTGTGCTACCGTTCACTCTTACCTATACCTTAATGGGGGAGTGGA	350
Rat Y2a	ACCCTGTGCCTGCCATTCACTCTTACCTATACCTTGTATGGGGGAGTGGA	350
Rat Y2b	ACCCTGTGCCTGCCATTCACTCTTACCTATACCTTGTATGGGGGAGTGGA	350

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FIGURE 10B

Hum Y2	AATGGGTCCCTGTCCCTGTGCCACCTGGTGCCCTATGCCCCAGGGCCCTGGCAG	400
Rat Y2a	AATGGGTCCAGTTTGTGCCATTGTGGTGCCCTATGCCCCAGGGTCTGGCAG	400
Rat Y2b	AATGGGTCCAGTTTGTGCCATTGTGGTGCCCTATGCCCCAGGGTCTGGCAG	400
Hum Y2	TACAAGTATCCACAATCACCTTGACAGTAATTGCCCTGGACCGGCACAGG	450
Rat Y2a	TACAAGTGTCCACAATAACTTTGACAGTCATTGCTTTGGACCGACATCGT	450
Rat Y2b	TACAAGTGTCCACAATAACTTTGACAGTCATTGCTTTGGACCGACATCGT	450
Hum Y2	TGCATCGTCTACCACTAGAGAGCAAGATCTCCAAGCGAATCAGCTTCCT	500
Rat Y2a	TGCATTGTCTACCACTGGAGAGCAAGATCTCCAAGCAATCAGCTTCCT	500
Rat Y2b	TGCATTGTCTACCACTGGAGAGCAAGATCTCCAAGCAATCAGCTTCCT	500
Hum Y2	GATTATTGGCTTGGCCTGGGGCATCAGTGCCCTGCTGGCAAGTCCCCCTGG	550
Rat Y2a	GATTATTGGCCTGGCGTGGGTGTCAAGCGCTCTGCTGGCAAGTCCCCCTTG	550
Rat Y2b	GATTATTGGCCTGGCGTGGGTGTCAAGCGCTCTGCTGGCAAGTCCCCCTTG	550
Hum Y2	CCATCTTCCGGGAGTATTTCGCTGATTGAGATCATCCCCGGACTTTGAGATT	600
Rat Y2a	CCATCTTCCGGGAGTACTCACTGATTGAGATTATTCTGACTTTGAGATT	600
Rat Y2b	CCATCTTCCGGGAGTACTCACTGATTGAGATTATTCTGACTTTGAGATT	600
Hum Y2	GTGGCCTGTACTGAAAAGTGGCCTGGCGAGGAGAAAGAGCATCTATGGCAC	650
Rat Y2a	GTAGCCTGTACTGAGAAATGGCCCCGGGAGGAGAGAGTGTGTACGGTAC	650
Rat Y2b	GTAGCCTGTACTGAGAAATGGCCCCGGGAGGAGAGAGTGTGTACGGTAC	650
Hum Y2	TGCTATAGTCTTTCTTCCCTTGTGATCTTGTATGTTTTCCTCTCTGGGCA	700
Rat Y2a	AGTCTACAGCCCTTCCACCCCTGCTAATCCTCTACGTTTTCCTCTCTGGGCA	700
Rat Y2b	AGTCTACAGCCCTTCCACCCCTGCTAATCCTCTACGTTTTCCTCTCTGGGCA	700

FIGURE 10C

Hum Y2	TTATATCATTTTCTACACTCGCATTTGGAGTAAATTGAAGAACCATGTC	750
Rat Y2a	TCATATCTTTCTCTACACCCGGATCTGGAGTAAAGCTAAAGAACCACTGTT	750
Rat Y2b	TCATATCTTTCTCTACACCCGGATCTGGAGTAAAGCTAAAGAACCACTGTT	750
Hum Y2	AGTCCTGGAGCTGCAAAATGACCACACTACCATCAGCGAAGGCACAAAAACAC	800
Rat Y2a	AGTCCTGGAGCTGCAAGTGACCATTACCATCAGCGAAGGCACAAAAACGAC	800
Rat Y2b	AGTCCTGGAGCTGCAAGTGACCATTACCATCAGCGAAGGCACAAAAATGAC	800
Hum Y2	CAAAATGCTGGTGTGTGGTGGTGTGTTGCGGTTCAGCTGGCTGCCCTC	850
Rat Y2a	CAAAATGCTCGTGTGCGTGGTAGTGGTGTGTTGCAGTCAGCTGGCTGCCCC	850
Rat Y2b	CAAAATGCTCGTGTGCGTGGTAGTGGTGTGTTGCAGTCAGCTGGCTGCCCC	850
Hum Y2	TCCATGCCCTTCCAGCTTGCCGTTGACATTGACAGCCAGGTCTTGGACCTG	900
Rat Y2a	TCCATGCCCTTCCAACTTGCTGTGGACATCGACAGCCATGTCTTGGACCTG	900
Rat Y2b	TCCATGCCCTTCCAACTTGCTGTGGACATCGACAGCCATGTCTTGGACCTG	900
Hum Y2	AAGGAGTACAAACTCATCTTCACAGTGTTCACATCATCGCCATGTGCTC	950
Rat Y2a	AAGGAGTACAAACTCATCTTCACCGTGTTCACATTTATTCGGATGTGCTC	950
Rat Y2b	AAGGAGTACAAACTCATCTTCACCGTGTTCACATTTATTCGGATGTGCTC	950
Hum Y2	CACCTTTGCCAATCCCCCTTCTCTATGGCTGGATGAACAGCAACTACAGAA	1000
Rat Y2a	CACCTTCGCCAACCCTTCTCTATGGCTGGATGAACAGCAACTACAGAA	1000
Rat Y2b	CACCTTCGCCAACCCTTCTCTATGGCTGGATGAACAGCAACTACAGAA	1000
Hum Y2	AGGCTTTCCTCTCGGCCCTTCCGCTGTGAGCAGCGGTTGGATGCCATTAC	1050
Rat Y2a	AAGCTTTCCTCTCAGCCCTTCCGCTGTGAGCAGAGGTTGGATGCCATTAC	1050
Rat Y2b	AAGCTTTCCTCTCAGCCCTTCCGCTGTGAGCAGAGGTTGGATGCCATTAC	1050

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FIGURE 10D

Hum Y2	TCTGAGGTGTCCGTGACATTCAAGGGCTAAAAAGAACCTGGAGGTCAGAAA	1100
Rat Y2a	TCGGAGGTGTCCATGACCTTCAAGGGCTAAAAAGAACCTGGAAAGTCAAAAA	1100
Rat Y2b	TCGGAGGTGTCCATGACCTTCAAGGGCTAAAAAGAACCTGGAAAGTCAAAAA	1100
Hum Y2	GAACAGTGGCCCCCAATGACTCTTTTCACAGAGGCTACCAATGTCTAA	1146
Rat Y2a	GAACAATGGCCTCACTGACTCTTTTTCAGAGGCCACCAACGTGTAA	1146
Rat Y2b	GAACAATGGCCTCACTGACTCTTTTTCAGAGGCCACCAACGTGTAA	1146

FIGURE 11A

FIGURE 11A
FIGURE 11B

Hum Y2	MGPIGAEADENQTV	EEEMKVEQYGP.QTTPRGELVPDPEPELIDSTKLIEV	49
Rat Y2a	MGPLGAEADENQTV	EVKVEFYGSGPTTPRGELPPDPEPELIDSTKLVEV	49
Rat Y2b	MGPLGAEADENQTV	EVKVEFYGSGPTTPRGELPPDPEPELIDSTKLVEV	49
Hum Y2	QVVLILAYCSII	LLGVIGNSLVIHVVI KFKSMRTVTN FFIANLAVADLLV	99
Rat Y2a	QVVLILAYCSII	LLGVVGNLSVIHVVI KFKSMRTVTN FFIANLAVADLLV	99
Rat Y2b	QVVLILAYCSII	LLGVVGNLSVIHVVI KFKSMRTVTN FFIANLAVADLLV	99
Hum Y2	NTLCLPFTLT	YTLMGWKMPVLCH LVPYAQGLAVQVSTITLTIVIAL DRH	149
Rat Y2a	NTLCLPFTLT	YTLMGWKMPVLCH LVPYAQGLAVQVSTITLTIVIAL DRH	149
Rat Y2b	NTLCLPFTLT	YTLMGWKMPVLCH LVPYAQGLAVQVSTITLTIVIAL DRH	149
Hum Y2	RCIVYHLESKISKRI	SFLIIGLAWGISALLASPLAIF REYSLIEIIPDFF	199
Rat Y2a	RCIVYHLESKISKQI	SFLIIGLAWGVSALLASPLAIF REYSLIEIIPDFF	199
Rat Y2b	RCIVYHLESKISKQI	SFLIIGLAWGVSALLASPLAIF REYSLIEIIPDFF	199
Hum Y2	IVACTEKWPGEESKIYGT	VYSLSSLLILYVPLPLGIISFSYT RIWSKLKNH	249
Rat Y2a	IVACTEKWPGEESKSVYGT	VYSLSTLLILYVPLPLGIISFSYT RIWSKLKNH	249
Rat Y2b	IVACTEKWPGEESKSVYGT	VYSLSTLLILYVPLPLGIISFSYT RIWSKLKNH	249
Hum Y2	VSPGAANDHYHQRRQKTKM	LVCVVVVFAVSWLPLHAFQLAVDI DSQVLD	299
Rat Y2a	VSPGAASDHYHQRRHKTKM	LVCVVVVFAVSWLPLHAFQLAVDI DSHVLD	299
Rat Y2b	VSPGAASDHYHQRRHKTKM	LVCVVVVFAVSWLPLHAFQLAVDI DSHVLD	299

FIGURE 11B

Hum Y2	LKEYKL	IFTVFHIIAMCSTFANPLLYGWM	NSNYRKAFLSAFRCQRLDAI	349
Rat Y2a	LKEYKL	IFTVFHIIAMCSTFANPLLYGWM	NSNYRKAFLSAFRCQRLDAI	349
Rat Y2b	LKEYKL	IFTVFHIIAMCSTFANPLLYGWM	NSNYRKAFLSAFRCQRLDAI	349
Hum Y2	HSEVSVTFKAKKNLEVRKNSGPNDSFTEATNV			381
Rat Y2a	HSEVSMTFKAKKNLEVKKNNGLTDSFSEATNV			381
Rat Y2b	HSEVSMTFKAKKNLEVKKNNGLTDSFSEATNV			381

FIGURE 12C

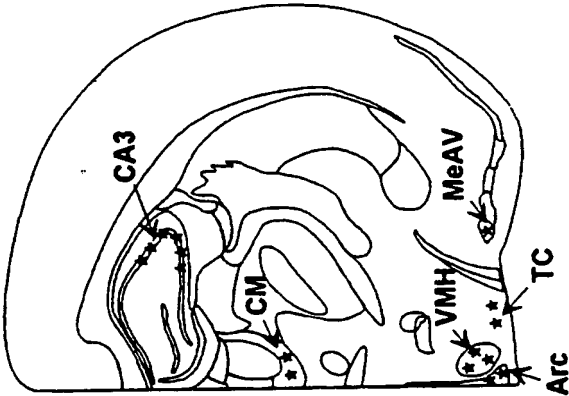


FIGURE 12B

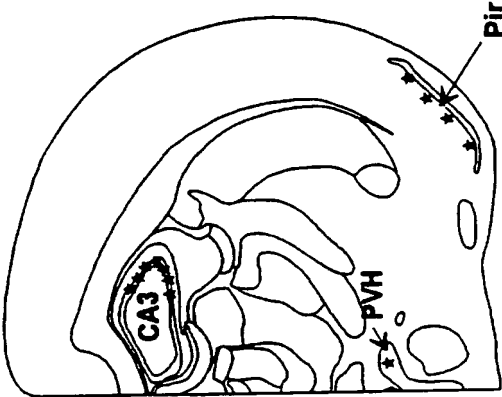
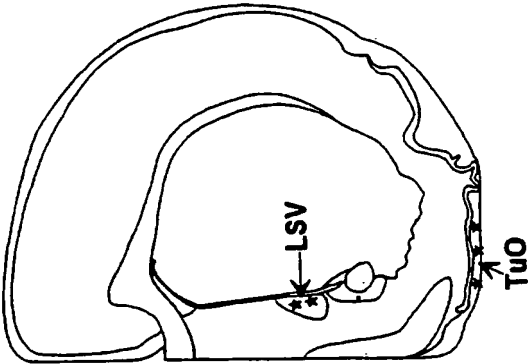


FIGURE 12A



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FIGURE 12F

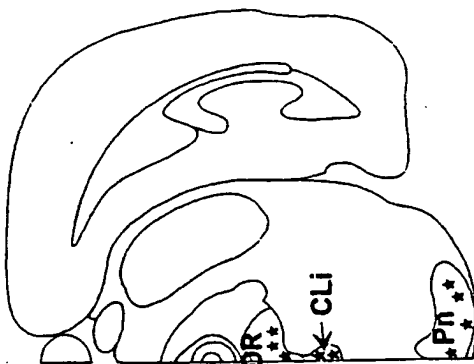


FIGURE 12E

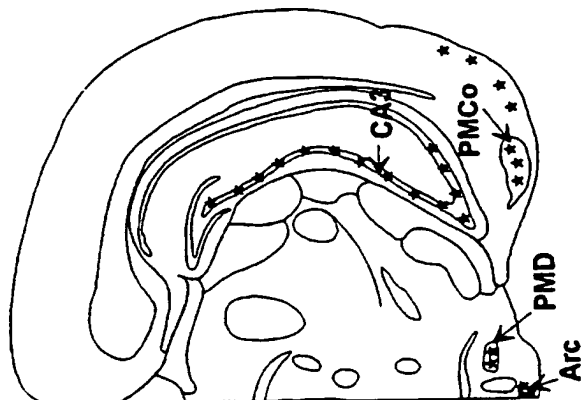
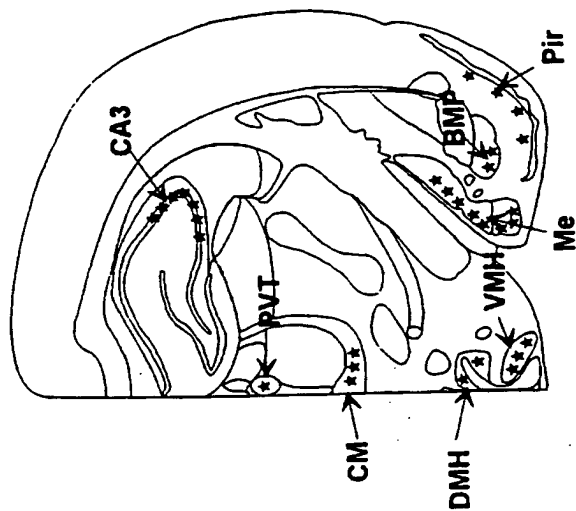


FIGURE 12D



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FIGURE 12G

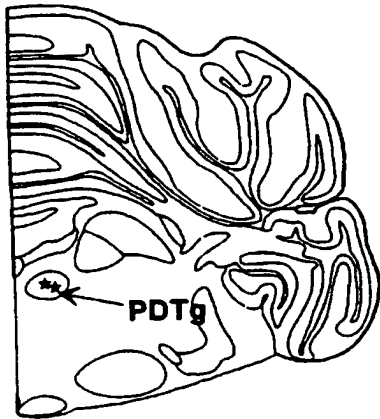
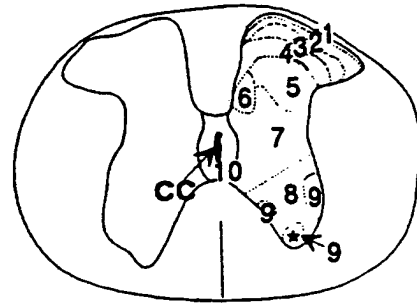


FIGURE 12H



Cervical Spinal Cord

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FIGURE 13A

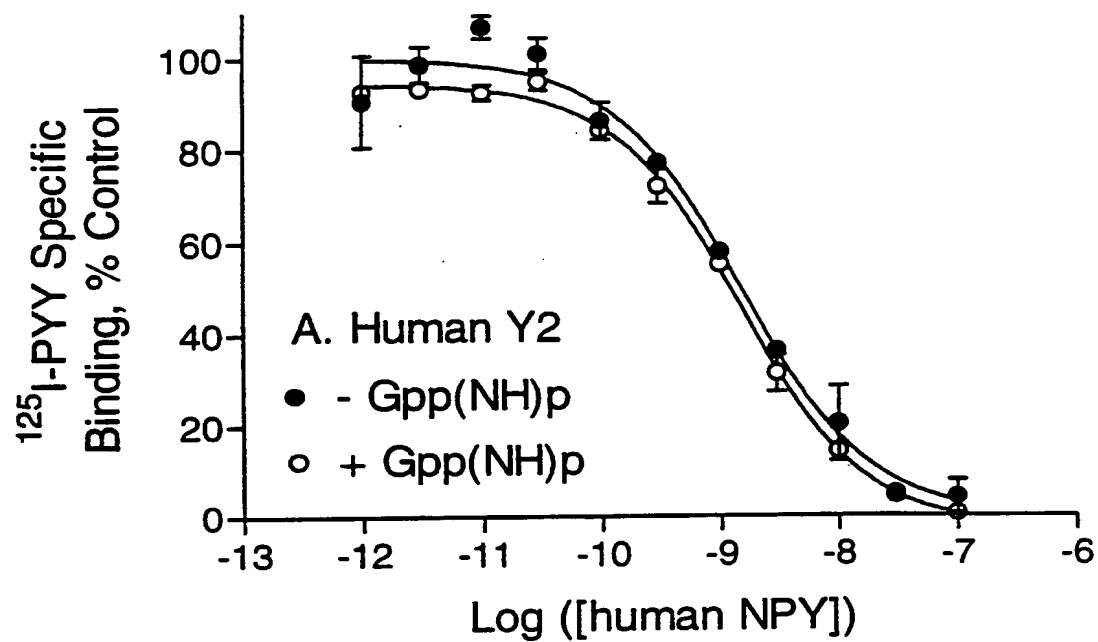
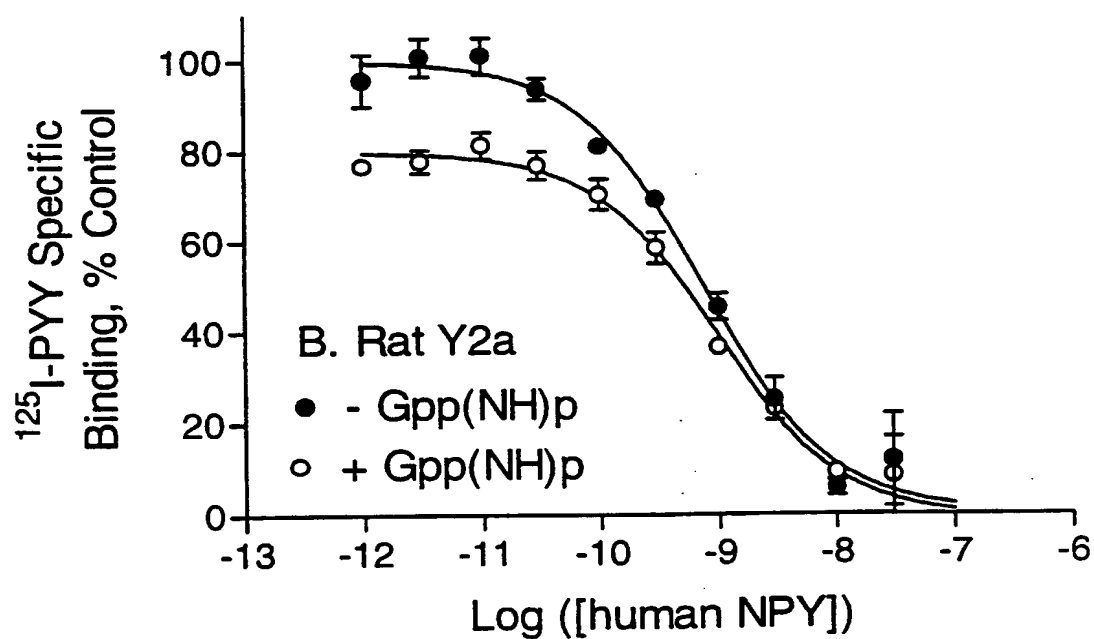
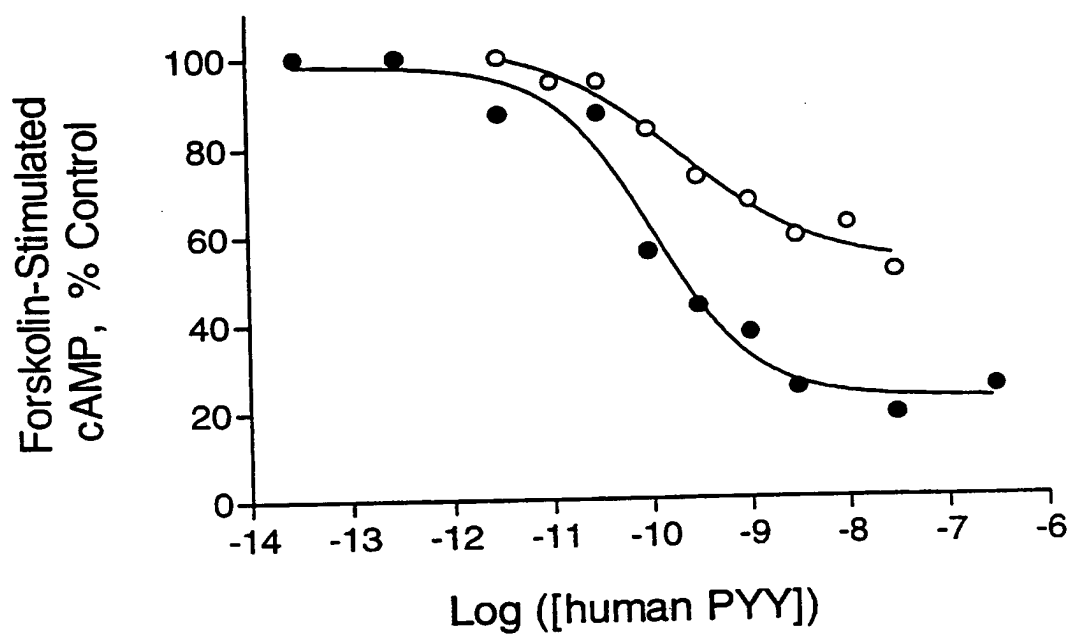


FIGURE 13B



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FIGURE 14



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FIGURE 15A

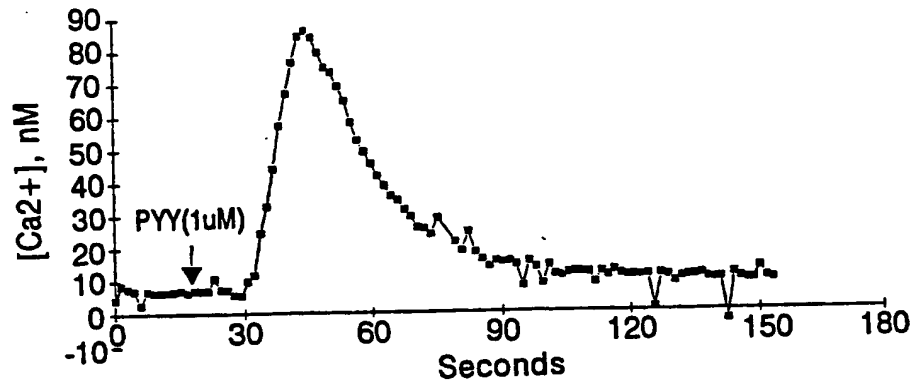


FIGURE 15B

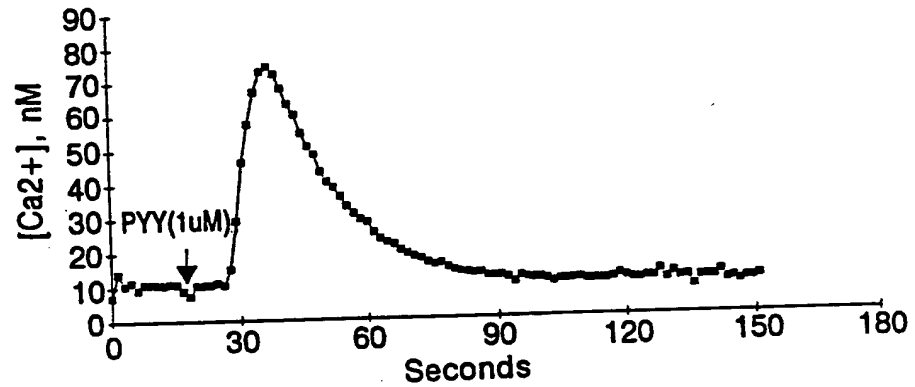
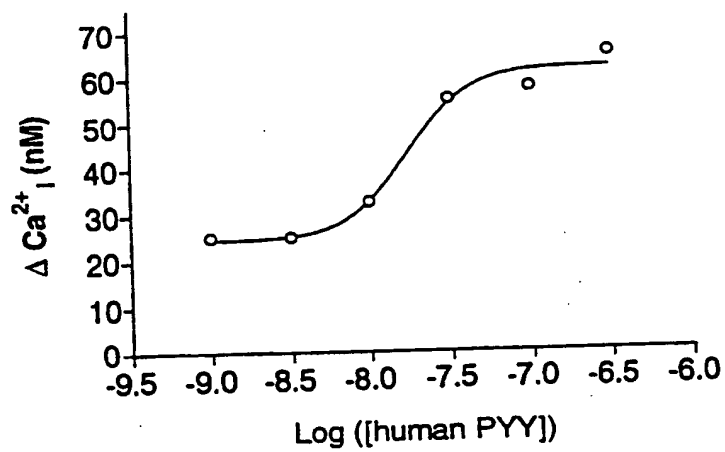
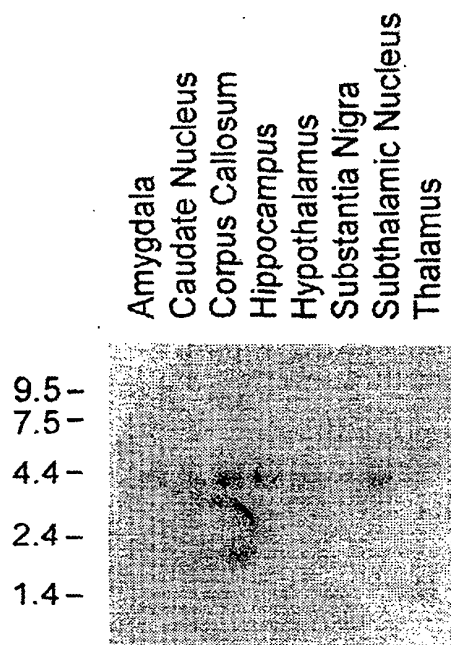


FIGURE 15C



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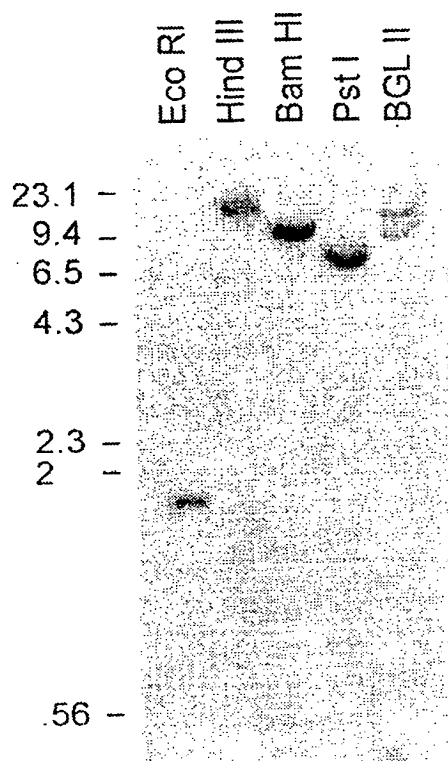
FIGURE 16



SUBSTITUTE SHEET (RULE 26)

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FIGURE 17



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FIGURE 18B

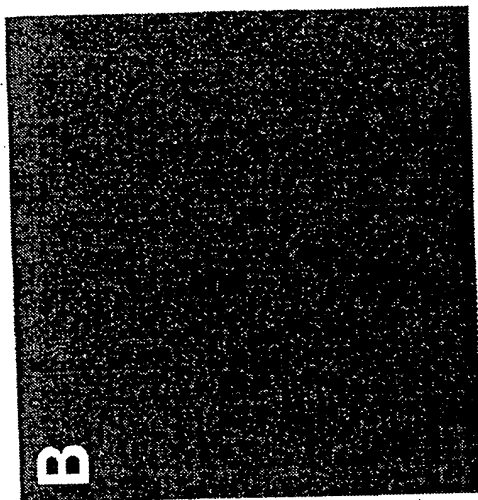


FIGURE 18A

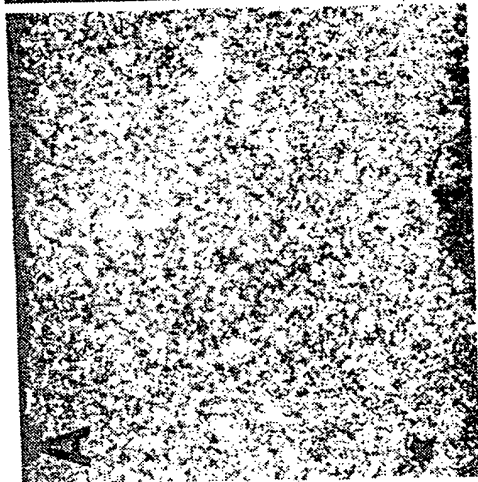


FIGURE 18D

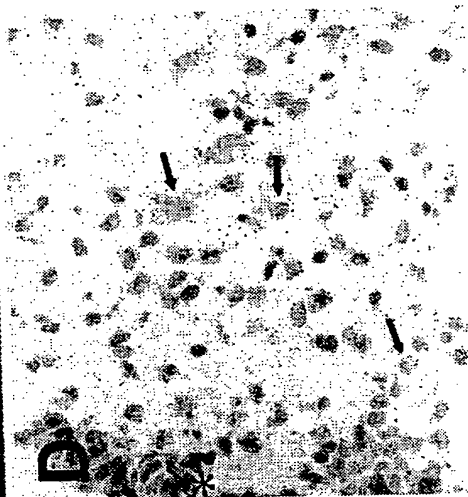
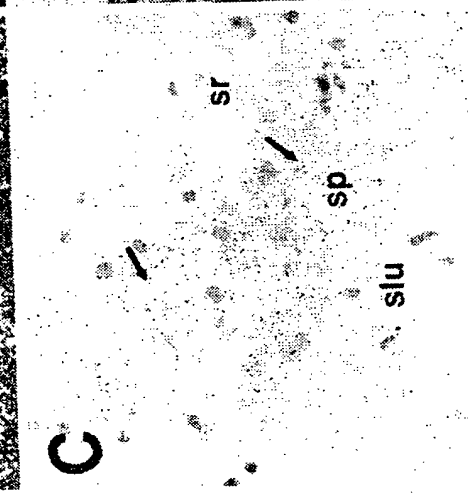


FIGURE 18C



SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/01469

A. CLASSIFICATION OF SUBJECT MATTER		
IPC(6) :Please See Extra Sheet. US CL :Please See Extra Sheet. According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/69.1, 70.1, 70.3, 71.1, 172.1, 240.1, 240.2, 320.1; 536/23.1, 23.5, 24.31; 530/350		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS; STN files Biosis, Medline, EMBASE, CA, WPIDS; search terms include: neuropeptide Y, NPY, Y1, Y2 (all with receptor#); sequence search.		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Annals of the New York Academy of Sciences, Volume 611, issued 15 November 1990, A. Inui et al, "Peptide YY Receptors in Mammalian and Avian Brains", pages 350-352, see entire document.	1-42, 122, 156
Y	Neuroscience Letters, Volume 140, issued 1992, J. Narvaez et al, "Intracerebroventricularly Administered Pertussis Toxin Blocks the Central Vasopressor Action of Neuropeptide Y(13-36) in the Awake Unrestrained Male Rat", pages 273-276, see entire document.	1-42, 122, 156
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents:	*T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *G document member of the same patent family	
*A document defining the general state of the art which is not considered to be of particular relevance		
*E earlier document published on or after the international filing date		
*L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		
*O document referring to an oral disclosure, use, exhibition or other means		
*P document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search 17 APRIL 1995	Date of mailing of the international search report 16 MAY 1995	
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer ARIE M. MICHELSON, PH.D. Telephone No. (703) 308-0196	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/01469

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Brain Research, Volume 596, issued 1992, C. Blasquez et al, "Neuropeptide Y Inhibits α -MSH Release from Rat Hypothalamic Slices Through a Pertussis Toxin-sensitive G Protein", pages 163-168, see entire document.	1-42, 122, 156
Y	Life Sciences, Volume 50, issued 1991, C. Wahlestedt et al, "Identification of Cultured Cells Selectively Expressing Y1-, Y2-, or Y3-Type Receptors for Neuropeptide Y/Peptide YY", pages PL-7-PL-12, see entire document.	1-42, 122, 156
Y	Journal of Biological Chemistry, Volume 266, Number 35, issued 15 December 1991, S. Sheikh et al, "Solubilization and Affinity Purification of the Y ₂ Receptor for Neuropeptide Y and Peptide YY from Rabbit Kidney", pages 23959-23966, see entire document.	1-42, 122, 156
Y	Annals of the New York Academy of Sciences, Volume 611, issued 15 November 1990, C. Wahlestedt et al, "Neuropeptide Y Receptor Subtypes, Y1 and Y2", pages 7-25, see pages 12-16 and 19-21.	1-42, 122, 156

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/01469

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-42, 122 and 156

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/01469

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 5/10, 5/16, 7/01, 15/00, 15/09, 15/10, 15/11, 15/12, 15/16, 15/63; C07H 21/00, 21/04; C07K 14/00, 14/705, 14/72

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

435/69.1, 70.1, 70.3, 71.1, 172.1, 240.1, 240.2, 320.1; 536/23.1, 23.5, 24.31; 530/350

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claims 1-42, 122 and 156, drawn to nucleic acids, probes and corresponding proteins, classified in U.S. Class 435, subclass 69.1, for example.

Group II, claims 43-45 and 51-55, drawn to antisense oligonucleotides, classified in U.S. Class 536, subclass 23.1; Class 514, subclass 44.

Group III, claims 46-50 and 56, drawn to antibodies, classified in U.S. Class 530, subclass 387.1.

Group IV, claims 57-62, drawn to transgenic animals, classified in U.S. Class 800, subclass 2.

Group V, claims 63-72, 74-87, 89-90, 98-115 and 117-118, drawn to binding assays, classified in U.S. Class 436, subclass 501.

Group VI, claims 73, 92 and 93, drawn to ligands, classified in U.S. Class 532, subclass 1, for example.

Group VII, claims 88, 91, 116 and 119, drawn to cells, classified in U.S. Class 435, subclass 240.1.

Group VIII, claims 94-95, 151 and 152, drawn to agonists, classified in U.S. Class 514, subclass 1.

Group IX, claims 96-97, 147 and 148, drawn to antagonists, classified in U.S. Class 514, subclass 1.

Group X, claims 120-121, drawn to drugs, classified in U.S. Class 514, subclass 1.

Group XI, claims 123-124, and 153, drawn to methods of treatment with agonists, classified in U.S. Class 514, subclass 1.

Group XII, claims 125-126, 149 and/or 127-135, drawn to methods of treatment with antagonists, classified in U.S. Class 514, subclass 1.

Group XIII, claim 136 and/or claims 138-142, drawn to methods of treatment with antibodies, classified in U.S. Class 424, subclass 85.8.

Group XIV, claim 137 and/or claims 138-142, drawn to methods of treatment with antisense oligonucleotides, classified in U.S. Class 514, subclass 44.

Group XV, claim 143, drawn to method of detection using antibodies, classified in U.S. Class 436, subclass 501.

Group XVI, claims 144-145, drawn to methods of determining physiological effects using transgenic animals, classified in U.S. Class 424, subclass 9.

Group XVII, claims 154-155, drawn to methods of diagnosis using nucleic acid probes, classified in U.S. Class 435, subclass 6.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/01469

Group XVIII, claim 146, drawn to method for identifying antagonists using transgenic animals, classified in U.S. Class 424, subclass 9.

Group XIX, claim 150, drawn to method for identifying agonists using transgenic animals, classified in U.S. Class 424, subclass 9.

The inventions listed as Groups I-XIX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features; i.e., the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept, for the following reasons:

Groups I-IV and VI-X are materially distinct compositions of matter that are distinguished, each from the other, by their special technical features:

The polynucleotides and polypeptides of Group I, the antisense oligonucleotides of Group II, the antibodies of Group III, the transgenic animals of Group IV, the ligands of Group VI, the cells of Group VII, the agonists of Group VIII, the antagonists of Group XIX, and the drugs of Group X have materially different structures and functions.

The compositions of Groups I-IV and VI-X are not restricted for use in the methods of Groups V and XI-XIX, but can be used for materially different purposes, or at least for a single method from among those listed in Groups V and XI-XIX.

Groups V and XI-XIX are materially distinct methods which are distinguished, each from the other, by their process steps. The process steps accomplish materially distinct purposes and these special technical features do not link the methods as to form a single inventive concept.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

Drugs; agonists; antagonists; antibodies; and antisense oligonucleotides.

The claims are deemed to correspond to the species listed above in the following manner:

Claim 124: method employing agonist; Claim 126: method employing antagonist; Claim 136: method employing antisense oligonucleotides; Claim 137: method employing antibodies.

The following claims are generic: 123 (claiming either of the species of drugs or agonists); 125 and 127-135 (claiming either of the species of drugs or antagonists); 138-142 (claiming either of the species of antibodies or antisense oligonucleotides).

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: The drugs, agonists, antagonists, antibodies and antisense oligonucleotides are materially different compositions of matter that are distinguished, each from the other, by their special technical features, including their materially different structures and functions.

Accordingly, the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.